

## SEQUENCE LISTING

10/511989

New Seq. List w/P

<110> Ting, Jenny  
 Linhoff, Michael  
 Harton, Johnathan  
 Williams, Kristi  
 Lich, John  
 O'Connor, William  
 Moore, Christopher  
 Davis, Beckley  
 Brickey, W. Jane  
 Conti, Brian  
 Zhang, Jinghua  
 Zhu, Xin-Sheng

<120> CATERPILLER GENE FAMILY

<130> 5470-368

<140> US 10/511,989  
<141> 2004-10-20

<150> PCT/US03/13562  
<151> 2003-04-30

<150> US 60/376,626  
<151> 2002-04-30

<160> 187

<170> PatentIn version 3.3

<210> 1  
<211> 3731  
<212> DNA  
<213> Homo sapiens

<400> 1  
atttgtgagt gggcagggc aggagggAAC tgaagagtGA gaaAGCATTa ttTCAGCAAA 60  
aggTCTTCC TCCCTTGCTC actCCTCCAA ccACTGGCTC agCCTCTCCG cccgctgcct 120  
gtGAATGATG caatGGAAGG tGTGCTGGGG TCGCCCTGTG TCCCgtgcAt aggAGCATCT 180  
cAGCCTCCAG gTCCTCTCCT ttggggCTTA CGGCACCCCCC atGCTACGAA CCgCAGGcAG 240  
ggACGGCCTC TGTcgCCTGT ccACCTACTT ggaAGAActC gagGCTGTgg aactGAAGAA 300  
gttcaAGTta tacctgggGA ccgCgAcAGA gctgggAGAA ggcaAGAtCC cctgggGAAG 360  
catggagaAG gCCGGTCCCC TggAAATGGC ccAGCTGCTC AtCACCCACT tcgggCcAGA 420  
ggaggCCTGG aggttggCTC tcAGCACCTT tgAGCggATA AACAGGAAGG acCTGTGGGA 480  
gagaggACAG agAGAGGACC TggTgAgGGA tacCCACCTT ggtggCCCGT CCTCActTGG 540  
gaaccAGTCA acATGcCTTC TggAAGTCTC tCTTGTCACT ccaAGAAAAG AtCCCAggA 600  
aacCTACAGG gACTATGTCC gcAGGAAATT ccGGCTCATG gaAGACCGCA AtGCGCGCCT 660  
aggGGAATGT gtCAACCTCA gCcAccGGTA cacCCGGCTC ctGCTGGTGA aggAGCActC 720

aaacccatg caggtccagc agcagcttct ggacacaggc cggggacacg cgaggaccgt 780  
ggcacccag gctagccccca tcaagataga gaccctttt gagccagacg aggagcgccc 840  
cgagccaccg cgacccgtgg tcatgcaagg cgccgcaggg ataggcaagt ccatgctggc 900  
acacaaggtg atgctggact gggccggacgg gaagctttc caaggcagat ttgattatct 960  
cttctacatc aactgcaggg agatgaacca gagtgccacg gaatgcagca tgcaagac 1020  
catcttcagc tgctggcctg agcccagcgc gcctctccag gagtcatcc gagttcccg 1080  
gcgcctcctt ttcatcatcg acggcttcga tgagctcaag cttctttcc acgtcctca 1140  
gggaccctgg tgccctctgct gggaggagaa acggcccacg gagctgcttc ttaacagctt 1200  
aattcggaaag aagctgctcc ctgagctatc tttgctcatc accacacggc ccacggctt 1260  
ggagaagctc caccgtctgc tggagcaccc caggcatgtg gagatcctgg gcttctctg 1320  
ggcagaaaagg aaggaatact tctacaagta tttccacaat gcagagcagg cgggccaagt 1380  
cttcaattac gtgagggaca acgagcctct cttcaccatg tgcttcgtcc ccctggtgt 1440  
ctgggtggtg tgtacctgcc tccagcagca gctggagggt gggggctgt tgagacagac 1500  
gtccaggacc accactgcag tgtacatgct ctacctgctg agtctgatgc aacccaagcc 1560  
gggggccccg cgcctccagc ccccacccaa ccagagaggg ttgtgctcct tggcggcaga 1620  
tgggctctgg aatcagaaaa tcctatttga ggagcaggac ctccggaagc acggccctaga 1680  
cggggaagac gtctctgcct tcctcaacat gaacatttc cagaaggaca tcaactgtga 1740  
gaggtactac agttcatcc acttgagttt ccaggaattc tttgcagcta tgtactatat 1800  
cctggacgag ggggagggcg gggcaggccc agaccaggac gtgaccaggc tggaccga 1860  
gtacgcgttt tctgaaagga gcttcctggc actcaccagc cgcttcctgt ttggactcct 1920  
gaacgaggag accaggagcc acctggagaa gagtctctgc tggaggctc cgccgcacat 1980  
caagatggac ctgttgcagt ggatccaaag caaagctcag agcgcacggct ccaccctgca 2040  
gcagggtctcc ttggagttct tcagctgctt gtacgagatc caggaggagg agtttatcca 2100  
gcaggccctg agccacttcc aggtgatcgt ggtcagcaac attgcctcca agatggagca 2160  
catggtctcc tcgttctgtc tgaagcgctg caggagcggc caggtgctgc acttgtatgg 2220  
cgccacccatc agcgcggacg gggaaagaccc cgccgagggtc tccgcaggag cgacacacgt 2280  
gttgggtcag ctcagaccag agaggaccgt tctgctggac gcctacagt aacatctggc 2340  
agcggccctg tgcaccaatc caaacctgat agagctgtct ctgtaccgaa atgcctggg 2400  
cagccggggg gtgaagctgc tctgtcaagg actcagacac cccaaactgca aacttcagaa 2460  
cctgaggctg aagaggtgcc gcacatccatc ctcagccctgc gaggacccctt ctgcagctct 2520

catagccaat	aagaatttga	caaggatgga	tctcagtggc	aacggcggttgc	gattcccagg	2580
catgatgctg	ctttgcgagg	gcctgcggca	tccccagtc	aggctgcaga	tgattcagtt	2640
gaggaagtgt	cagctggagt	ccggggcttgc	tcaggagatg	gcttctgtgc	tcggcaccaa	2700
cccacatctg	gttgagttgg	acctgacagg	aaatgcactg	gaggatttgg	gcctgagggtt	2760
actatgccag	ggactgaggc	acccagtctg	cagactacgg	actttgtggc	tgaagatctg	2820
ccgcctcact	gctgctgcct	gtgacgagct	ggcctcaact	ctcagtgtga	accagagcct	2880
gagagagctg	gacctgagcc	tgaatgagct	gggggacac	gggtgctgc	tgctgtgtga	2940
gggcctcagg	catcccacgt	gcaagctcca	gaccctgcgg	ttgggcatct	gccggctggg	3000
ctctgcgc	tgtgagggtc	tttctgtggt	gctccaggcc	aaccacaacc	tccggagct	3060
ggacttgagt	ttcaacgacc	tgggagactg	gggcctgtgg	ttgctggctg	aggggctgca	3120
acatcccgcc	tgcagactcc	agaaactgtg	gctggatagc	tgtggcctca	cagccaaggc	3180
tttgtgagaat	ctttacttca	ccctggggat	caaccagacc	ttgaccgacc	tttacctgac	3240
caacaacgcc	ctaggggaca	caggtgtccg	actgcttgc	aagcggctga	gccatcctgg	3300
ctgcaaactc	cgagtcctct	ggttatttgg	gatggacctg	aataaaatga	cccacagtag	3360
gttggcagcg	cttcgagtaa	caaaaccta	tttggacatt	ggctgctgaa	tggtcctatc	3420
tgctggctct	cccctgagat	ctggacagag	gaagatggg	gggtgctcat	cacccccc	3480
gcataatgat	cagcctcctt	cctagagaca	gactcatgca	gattgagatc	aaaagtccct	3540
ctgcttggga	tcaaattaat	gttgacaga	gctggccagg	cgtggggct	catgtatgta	3600
atcctagcac	ttcgagaggc	cgagggcaggt	ggatcacgag	gtcaggagtt	tgagattagc	3660
ctggccaaga	tggtaaaacc	ctgtctctac	taaaaataaa	aaaaaattag	ccagaaaaaa	3720
aaaaaaaaaa	a					3731

<210> 2  
 <211> 1062  
 <212> PRT  
 <213> Homo sapiens

<400> 2

Met	Leu	Arg	Thr	Ala	Gly	Arg	Asp	Gly	Leu	Cys	Arg	Leu	Ser	Thr	Tyr
1									10					15	

Leu	Glu	Glu	Leu	Glu	Ala	Val	Glu	Leu	Lys	Lys	Phe	Lys	Leu	Tyr	Leu
								20		25				30	

Gly	Thr	Ala	Thr	Glu	Leu	Gly	Glu	Gly	Lys	Ile	Pro	Trp	Gly	Ser	Met
									35		40			45	

Glu Lys Ala Gly Pro Leu Glu Met Ala Gln Leu Leu Ile Thr His Phe  
50 55 60

Gly Pro Glu Glu Ala Trp Arg Leu Ala Leu Ser Thr Phe Glu Arg Ile  
65 70 75 80

Asn Arg Lys Asp Leu Trp Glu Arg Gly Gln Arg Glu Asp Leu Val Arg  
85 90 95

Asp Thr Pro Pro Gly Gly Pro Ser Ser Leu Gly Asn Gln Ser Thr Cys  
100 105 110

Leu Leu Glu Val Ser Leu Val Thr Pro Arg Lys Asp Pro Gln Glu Thr  
115 120 125

Tyr Arg Asp Tyr Val Arg Arg Lys Phe Arg Leu Met Glu Asp Arg Asn  
130 135 140

Ala Arg Leu Gly Glu Cys Val Asn Leu Ser His Arg Tyr Thr Arg Leu  
145 150 155 160

Leu Leu Val Lys Glu His Ser Asn Pro Met Gln Val Gln Gln Gln Leu  
165 170 175

Leu Asp Thr Gly Arg Gly His Ala Arg Thr Val Gly His Gln Ala Ser  
180 185 190

Pro Ile Lys Ile Glu Thr Leu Phe Glu Pro Asp Glu Glu Arg Pro Glu  
195 200 205

Pro Pro Arg Thr Val Val Met Gln Gly Ala Ala Gly Ile Gly Lys Ser  
210 215 220

Met Leu Ala His Lys Val Met Leu Asp Trp Ala Asp Gly Lys Leu Phe  
225 230 235 240

Gln Gly Arg Phe Asp Tyr Leu Phe Tyr Ile Asn Cys Arg Glu Met Asn  
245 250 255

Gln Ser Ala Thr Glu Cys Ser Met Gln Asp Leu Ile Phe Ser Cys Trp  
260 265 270

Pro Glu Pro Ser Ala Pro Leu Gln Glu Leu Ile Arg Val Pro Glu Arg  
275 280 285

Leu Leu Phe Ile Ile Asp Gly Phe Asp Glu Leu Lys Pro Ser Phe His  
290 295 300

Asp Pro Gln Gly Pro Trp Cys Leu Cys Trp Glu Glu Lys Arg Pro Thr  
305 310 315 320

Glu Leu Leu Leu Asn Ser Leu Ile Arg Lys Lys Leu Leu Pro Glu Leu  
325 330 335

Ser Leu Leu Ile Thr Thr Arg Pro Thr Ala Leu Glu Lys Leu His Arg  
340 345 350

Leu Leu Glu His Pro Arg His Val Glu Ile Leu Gly Phe Ser Glu Ala  
355 360 365

Glu Arg Lys Glu Tyr Phe Tyr Lys Tyr Phe His Asn Ala Glu Gln Ala  
370 375 380

Gly Gln Val Phe Asn Tyr Val Arg Asp Asn Glu Pro Leu Phe Thr Met  
385 390 395 400

Cys Phe Val Pro Leu Val Cys Trp Val Val Cys Thr Cys Leu Gln Gln  
405 410 415

Gln Leu Glu Gly Gly Leu Leu Arg Gln Thr Ser Arg Thr Thr Thr  
420 425 430

Ala Val Tyr Met Leu Tyr Leu Leu Ser Leu Met Gln Pro Lys Pro Gly  
435 440 445

Ala Pro Arg Leu Gln Pro Pro Pro Asn Gln Arg Gly Leu Cys Ser Leu  
450 455 460

Ala Ala Asp Gly Leu Trp Asn Gln Lys Ile Leu Phe Glu Glu Gln Asp  
465 470 475 480

Leu Arg Lys His Gly Leu Asp Gly Glu Asp Val Ser Ala Phe Leu Asn  
485 490 495

Met Asn Ile Phe Gln Lys Asp Ile Asn Cys Glu Arg Tyr Tyr Ser Phe  
500 505 510

Ile His Leu Ser Phe Gln Glu Phe Phe Ala Ala Met Tyr Tyr Ile Leu  
515 520 525

Asp Glu Gly Glu Gly Ala Gly Pro Asp Gln Asp Val Thr Arg Leu

530

535

540

Leu Thr Glu Tyr Ala Phe Ser Glu Arg Ser Phe Leu Ala Leu Thr Ser  
545 550 555 560

Arg Phe Leu Phe Gly Leu Leu Asn Glu Glu Thr Arg Ser His Leu Glu  
565 570 575

Lys Ser Leu Cys Trp Lys Val Ser Pro His Ile Lys Met Asp Leu Leu  
580 585 590

Gln Trp Ile Gln Ser Lys Ala Gln Ser Asp Gly Ser Thr Leu Gln Gln  
595 600 605

Gly Ser Leu Glu Phe Phe Ser Cys Leu Tyr Glu Ile Gln Glu Glu Glu  
610 615 620

Phe Ile Gln Gln Ala Leu Ser His Phe Gln Val Ile Val Val Ser Asn  
625 630 635 640

Ile Ala Ser Lys Met Glu His Met Val Ser Ser Phe Cys Leu Lys Arg  
645 650 655

Cys Arg Ser Ala Gln Val Leu His Leu Tyr Gly Ala Thr Tyr Ser Ala  
660 665 670

Asp Gly Glu Asp Arg Ala Arg Cys Ser Ala Gly Ala His Thr Leu Leu  
675 680 685

Val Gln Leu Arg Pro Glu Arg Thr Val Leu Leu Asp Ala Tyr Ser Glu  
690 695 700

His Leu Ala Ala Ala Leu Cys Thr Asn Pro Asn Leu Ile Glu Leu Ser  
705 710 715 720

Leu Tyr Arg Asn Ala Leu Gly Ser Arg Gly Val Lys Leu Leu Cys Gln  
725 730 735

Gly Leu Arg His Pro Asn Cys Lys Leu Gln Asn Leu Arg Leu Lys Arg  
740 745 750

Cys Arg Ile Ser Ser Ser Ala Cys Glu Asp Leu Ser Ala Ala Leu Ile  
755 760 765

Ala Asn Lys Asn Leu Thr Arg Met Asp Leu Ser Gly Asn Gly Val Gly  
770 775 780

Phe Pro Gly Met Met Leu Leu Cys Glu Gly Leu Arg His Pro Gln Cys  
785                    790                    795                    800

Arg Leu Gln Met Ile Gln Leu Arg Lys Cys Gln Leu Glu Ser Gly Ala  
805                    810                    815

Cys Gln Glu Met Ala Ser Val Leu Gly Thr Asn Pro His Leu Val Glu  
820                    825                    830

Leu Asp Leu Thr Gly Asn Ala Leu Glu Asp Leu Gly Leu Arg Leu Leu  
835                    840                    845

Cys Gln Gly Leu Arg His Pro Val Cys Arg Leu Arg Thr Leu Trp Leu  
850                    855                    860

Lys Ile Cys Arg Leu Thr Ala Ala Ala Cys Asp Glu Leu Ala Ser Thr  
865                    870                    875                    880

Leu Ser Val Asn Gln Ser Leu Arg Glu Leu Asp Leu Ser Leu Asn Glu  
885                    890                    895

Leu Gly Asp Leu Gly Val Leu Leu Leu Cys Glu Gly Leu Arg His Pro  
900                    905                    910

Thr Cys Lys Leu Gln Thr Leu Arg Leu Gly Ile Cys Arg Leu Gly Ser  
915                    920                    925

Ala Ala Cys Glu Gly Leu Ser Val Val Leu Gln Ala Asn His Asn Leu  
930                    935                    940

Arg Glu Leu Asp Leu Ser Phe Asn Asp Leu Gly Asp Trp Gly Leu Trp  
945                    950                    955                    960

Leu Leu Ala Glu Gly Leu Gln His Pro Ala Cys Arg Leu Gln Lys Leu  
965                    970                    975

Trp Leu Asp Ser Cys Gly Leu Thr Ala Lys Ala Cys Glu Asn Leu Tyr  
980                    985                    990

Phe Thr Leu Gly Ile Asn Gln Thr Leu Thr Asp Leu Tyr Leu Thr Asn  
995                    1000                    1005

Asn Ala Leu Gly Asp Thr Gly Val Arg Leu Leu Cys Lys Arg Leu  
1010                    1015                    1020

Ser His Pro Gly Cys Lys Leu Arg Val Leu Trp Leu Phe Gly Met  
1025 1030 1035

Asp Leu Asn Lys Met Thr His Ser Arg Leu Ala Ala Leu Arg Val  
1040 1045 1050

Thr Lys Pro Tyr Leu Asp Ile Gly Cys  
1055 1060

<210> 3  
<211> 3563  
<212> DNA  
<213> Homo sapiens

<400> 3  
atggtgagt gggcagggc aggagggAAC tgaagagtGA gaaAGCATTa tttcAGcaAA 60  
aggTCTTCC TCCCTGCTC actCCTCAA CCACTGGCTC agCCTCTCCG cccgctgcct 120  
gtGAATGATG caATGGAAGG tGTGCTGGGG tcGCCtGTG tCCCGTGCAT aggAGCATCT 180  
cAGCCTCCAG GTCCTCTCCT ttGGGGCTTA CGGCACCCCCC atGCTACGAA CGCAGGGCAG 240  
ggacGGCCTC TGTGCGCTGT ccACCTACTT ggaAGAACTC gagGCTGTGG aactGAAGAA 300  
gttCAAGTTA tacCTGGGA CGCGACAGA gCTGGGAGAA ggCAAGATCC CCTGGGGAAg 360  
catGGAGAAG gCCGGTCCCC tggAAATGGC ccAGCTGCTC atCACCCACT tcGGGCCAGA 420  
ggaggCCTGG aggtTGGCTC tcAGCACCTT tgAGCGATA AACAGGAAGG acCTGTGGGA 480  
gagAGGACAG agAGAGGACC tggTGAGGGTA tacCCCACCT ggtGGCCCGT CCTCACTTGG 540  
gaaccAGTCA acATGCCTTC tgGAAGTCTC tCTTGTCACT ccaAGAAAAG atCCCCAGGA 600  
aacCTACAGG gACTATGTCC gcAGGAAATT ccGGCTCATG gaAGACCGCA atGCGCGCCT 660  
aggGGAATGT gtCAACCTCA GCCACCGTA CACCCGGCTC ctGCTGGTGA aggAGCACTC 720  
aaACCCCATG caggTCCAGC agCAGCTCT ggACACAGGC CGGGGACACG cgaggACCGT 780  
gggACACAG gCTAGCCCCA tcaAGATAGA gACCCTTTT gagCCAGACG aggAGCGCCC 840  
cgAGCCACCG CGCACCGTGG tcatGCAAGG CGCGGCAGGG atAGGCAAGT ccatGCTGGC 900  
acacaAGGTG atGCTGGACT gggCggACGG gaAGCTCTC CAAGGCAGAT ttGATTATCT 960  
cttCTACATC aactGCAGGG agATGAACCA gagTGCACAG gaATGCAGCA tgCAAGACCT 1020  
catCTTCAGC tgCTGGCCTG agCCCAgCGC GCCTCTCCAG gagCTCATCC gagTTCCCGA 1080  
gcgcCTCCtt ttCATCATCG acGGCTTCGA tgAGCTCAAG CCTTCTTCC acGATCCTCA 1140  
gggACCTGG tgCCCTGTCT gggAGGGAGAA acGGCCACG gagCTGCTTC ttaACAGCTT 1200  
aattCggAAg aagCTGCTCC ctGAGCTATC tttGCTCATC accACACGGC ccACGGCTT 1260

ggagaagctc caccgtctgc tggagcaccc caggcatgtg gagatcctgg gcttctctga	1320
ggcagaaagg aaggaatact tctacaagta tttccacaat gcagagcagg cgggccaagt	1380
cttcaattac gtgagggaca acgagcctct cttcaccatg tgcttcgtcc ccctggtgtg	1440
ctgggtggtg tgtacctgcc tccagcagca gctggagggt gggggctgt tgagacagac	1500
gtccaggacc accactgcag tgtacatgct ctacctgctg agtctgatgc aacccaagcc	1560
gggggccccg cgccctccagc ccccacccaa ccagagaggg ttgtgctcct tggcggcaga	1620
tgggctctgg aatcagaaaa tcctatttga ggagcaggac ctccggaagc acggcctaga	1680
cgggaaagac gtctctgcct tcctcaacat gaacatctc cagaaggaca tcaactgtga	1740
gaggtactac agcttcatcc acttgagttt ccaggaattc tttgcagcta tgtactatat	1800
cctggacgag ggggagggcg gggcaggccc agaccaggac gtgaccaggc tggactcct	1860
gtacgcgttt tctgaaagga gcttcctggc actcaccagc cgcttcctgt ttggactcct	1920
gaacgaggag accaggagcc acctggagaa gagtctctgc tggaaaggctc cgccgcacat	1980
caagatggac ctgttgcagt ggatccaaag caaagctcag agcgcacggct ccaccctgca	2040
cgagggctcc ttggagttct tcagctgctt gtacgagatc caggaggagg agtttatcca	2100
gcaggccctg agccacttcc aggtgatcgt ggtcagcaac attgcctcca agatggagca	2160
catggcttcc tcgttctgtc tgaagcgctg caggagcgcc caggtgctgc acttgtatgg	2220
cgccacctac agcgcggacg gggaaagaccg cgcgagggtgc tccgcaggag cgacacgct	2280
gttggcag ctcagaccag agaggaccgt tctgctggac gcctacagtgc aacatctggc	2340
agcggccctg tgcaccaatc caaacctgat agagctgtct ctgtaccgaa atgcctggg	2400
cagccggggg gtgaagctgc tctgtcaagg actcagacac cccaaactgca aacttcagaa	2460
cctgaggctg aagaggtgcc gcacactccag ctcagcctgc gaggacctct ctgcagctct	2520
catagccaat aagaatttga caaggatgga tctcagtgcc aacggcggtt gattccagg	2580
catgatgctg ctttgcgagg gcctgcggca tccccagtgc aggctgcaga tgattcagtt	2640
gaggaagtgt cagctggagt cggggcttg tcaggagatg gcttctgtgc tcggcaccaa	2700
cccacatctg gttgagttgg acctgacagg aaatgcactg gaggattgg gcctgaggtt	2760
actatgccag ggactgagggc acccagtctg cagactacgg actttgtggc tgaagatctg	2820
ccgcctcaact gctgctgcct gtgacgagct ggcctcaact ctcagtgatgc accagagcct	2880
gagagagctg gacctgagcc tgaatgagct gggggaccc tcggcaccaa tgctgtgtga	2940
gggcctcagg catcccacgt gcaagctcca gaccctgcgg ttgggcattt gccggctggg	3000
ctctgcccgc ttttgcgtgtt gctccaggcc aaccacaacc tccggagct	3060
ggacttgagt ttcaacgacc tgggagactg gggcctgtgg ttgctggctg aggggctgca	3120

acatccggcc tgcagactcc agaaaactgtg gtggttattt gggatggacc tgaataaaat 3180  
gacccacagt aggttggcag cgcttcgagt aacaaaacct tatttggaca ttggctgctg 3240  
aatggtccta tctgctggct ctccccctgag atctggacag aggaagatgg gagggtgctc 3300  
atcacccccc cagcataatg atcagcctcc ttccttagaga cagactcatg cagattgaga 3360  
tcaaaaagtcc ctctgcttgg gatcaaatta atgtttgaca gagctggcca ggcgtggtgg 3420  
ctcatgtatg taatccttagc acttcgagag gccgaggcag gtggatcacf aggtcaggag 3480  
ttttagatata gcctggccaa gatggtaaa ccctgtctct actaaaaata aaaaaaaaaatt 3540  
agccaggaaa aaaaaaaaaaaa aaa 3563

<210> 4  
<211> 1006  
<212> PRT  
<213> Homo sapiens

<400> 4

Met Leu Arg Thr Ala Gly Arg Asp Gly Leu Cys Arg Leu Ser Thr Tyr  
1 5 10 15

Leu Glu Glu Leu Glu Ala Val Glu Leu Lys Lys Phe Lys Leu Tyr Leu  
20 25 30

Gly Thr Ala Thr Glu Leu Gly Glu Gly Lys Ile Pro Trp Gly Ser Met  
35 40 45

Glu Lys Ala Gly Pro Leu Glu Met Ala Gln Leu Leu Ile Thr His Phe  
50 55 60

Gly Pro Glu Glu Ala Trp Arg Leu Ala Leu Ser Thr Phe Glu Arg Ile  
65 70 75 80

Asn Arg Lys Asp Leu Trp Glu Arg Gly Gln Arg Glu Asp Leu Val Arg  
85 90 95

Asp Thr Pro Pro Gly Gly Pro Ser Ser Leu Gly Asn Gln Ser Thr Cys  
100 105 110

Leu Leu Glu Val Ser Leu Val Thr Pro Arg Lys Asp Pro Gln Glu Thr  
115 120 125

Tyr Arg Asp Tyr Val Arg Arg Lys Phe Arg Leu Met Glu Asp Arg Asn  
130 135 140

Ala Arg Leu Gly Glu Cys Val Asn Leu Ser His Arg Tyr Thr Arg Leu  
145 150 155 160

Leu Leu Val Lys Glu His Ser Asn Pro Met Gln Val Gln Gln Leu  
165 170 175

Leu Asp Thr Gly Arg Gly His Ala Arg Thr Val Gly His Gln Ala Ser  
180 185 190

Pro Ile Lys Ile Glu Thr Leu Phe Glu Pro Asp Glu Glu Arg Pro Glu  
195 200 205

Pro Pro Arg Thr Val Val Met Gln Gly Ala Ala Gly Ile Gly Lys Ser  
210 215 220

Met Leu Ala His Lys Val Met Leu Asp Trp Ala Asp Gly Lys Leu Phe  
225 230 235 240

Gln Gly Arg Phe Asp Tyr Leu Phe Tyr Ile Asn Cys Arg Glu Met Asn  
245 250 255

Gln Ser Ala Thr Glu Cys Ser Met Gln Asp Leu Ile Phe Ser Cys Trp  
260 265 270

Pro Glu Pro Ser Ala Pro Leu Gln Glu Leu Ile Arg Val Pro Glu Arg  
275 280 285

Leu Leu Phe Ile Ile Asp Gly Phe Asp Glu Leu Lys Pro Ser Phe His  
290 295 300

Asp Pro Gln Gly Pro Trp Cys Leu Cys Trp Glu Glu Lys Arg Pro Thr  
305 310 315 320

Glu Leu Leu Leu Asn Ser Leu Ile Arg Lys Lys Leu Leu Pro Glu Leu  
325 330 335

Ser Leu Leu Ile Thr Thr Arg Pro Thr Ala Leu Glu Lys Leu His Arg  
340 345 350

Leu Leu Glu His Pro Arg His Val Glu Ile Leu Gly Phe Ser Glu Ala  
355 360 365

Glu Arg Lys Glu Tyr Phe Tyr Lys Tyr Phe His Asn Ala Glu Gln Ala  
370 375 380

Gly Gln Val Phe Asn Tyr Val Arg Asp Asn Glu Pro Leu Phe Thr Met

385

390

395

400

Cys Phe Val Pro Leu Val Cys Trp Val Val Cys Thr Cys Leu Gln Gln  
405 410 415

Gln Leu Glu Gly Gly Leu Leu Arg Gln Thr Ser Arg Thr Thr Thr  
420 425 430

Ala Val Tyr Met Leu Tyr Leu Leu Ser Leu Met Gln Pro Lys Pro Gly  
435 440 445

Ala Pro Arg Leu Gln Pro Pro Asn Gln Arg Gly Leu Cys Ser Leu  
450 455 460

Ala Ala Asp Gly Leu Trp Asn Gln Lys Ile Leu Phe Glu Glu Gln Asp  
465 470 475 480

Leu Arg Lys His Gly Leu Asp Gly Glu Asp Val Ser Ala Phe Leu Asn  
485 490 495

Met Asn Ile Phe Gln Lys Asp Ile Asn Cys Glu Arg Tyr Tyr Ser Phe  
500 505 510

Ile His Leu Ser Phe Gln Glu Phe Phe Ala Ala Met Tyr Tyr Ile Leu  
515 520 525

Asp Glu Gly Glu Gly Ala Gly Pro Asp Gln Asp Val Thr Arg Leu  
530 535 540

Leu Thr Glu Tyr Ala Phe Ser Glu Arg Ser Phe Leu Ala Leu Thr Ser  
545 550 555 560

Arg Phe Leu Phe Gly Leu Leu Asn Glu Glu Thr Arg Ser His Leu Glu  
565 570 575

Lys Ser Leu Cys Trp Lys Val Ser Pro His Ile Lys Met Asp Leu Leu  
580 585 590

Gln Trp Ile Gln Ser Lys Ala Gln Ser Asp Gly Ser Thr Leu Gln Gln  
595 600 605

Gly Ser Leu Glu Phe Phe Ser Cys Leu Tyr Glu Ile Gln Glu Glu Glu  
610 615 620

Phe Ile Gln Gln Ala Leu Ser His Phe Gln Val Ile Val Val Ser Asn  
625 630 635 640

Ile Ala Ser Lys Met Glu His Met Val Ser Ser Phe Cys Leu Lys Arg  
645 650 655

Cys Arg Ser Ala Gln Val Leu His Leu Tyr Gly Ala Thr Tyr Ser Ala  
660 665 670

Asp Gly Glu Asp Arg Ala Arg Cys Ser Ala Gly Ala His Thr Leu Leu  
675 680 685

Val Gln Leu Arg Pro Glu Arg Thr Val Leu Leu Asp Ala Tyr Ser Glu  
690 695 700

His Leu Ala Ala Ala Leu Cys Thr Asn Pro Asn Leu Ile Glu Leu Ser  
705 710 715 720

Leu Tyr Arg Asn Ala Leu Gly Ser Arg Gly Val Lys Leu Leu Cys Gln  
725 730 735

Gly Leu Arg His Pro Asn Cys Lys Leu Gln Asn Leu Arg Leu Lys Arg  
740 745 750

Cys Arg Ile Ser Ser Ala Cys Glu Asp Leu Ser Ala Ala Leu Ile  
755 760 765

Ala Asn Lys Asn Leu Thr Arg Met Asp Leu Ser Gly Asn Gly Val Gly  
770 775 780

Phe Pro Gly Met Met Leu Leu Cys Glu Gly Leu Arg His Pro Gln Cys  
785 790 795 800

Arg Leu Gln Met Ile Gln Leu Arg Lys Cys Gln Leu Glu Ser Gly Ala  
805 810 815

Cys Gln Glu Met Ala Ser Val Leu Gly Thr Asn Pro His Leu Val Glu  
820 825 830

Leu Asp Leu Thr Gly Asn Ala Leu Glu Asp Leu Gly Leu Arg Leu Leu  
835 840 845

Cys Gln Gly Leu Arg His Pro Val Cys Arg Leu Arg Thr Leu Trp Leu  
850 855 860

Lys Ile Cys Arg Leu Thr Ala Ala Ala Cys Asp Glu Leu Ala Ser Thr  
865 870 875 880

Leu Ser Val Asn Gln Ser Leu Arg Glu Leu Asp Leu Ser Leu Asn Glu  
885 890 895

Leu Gly Asp Leu Gly Val Leu Leu Cys Glu Gly Leu Arg His Pro  
900 905 910

Thr Cys Lys Leu Gln Thr Leu Arg Leu Gly Ile Cys Arg Leu Gly Ser  
915 920 925

Ala Ala Cys Glu Gly Leu Ser Val Val Leu Gln Ala Asn His Asn Leu  
930 935 940

Arg Glu Leu Asp Leu Ser Phe Asn Asp Leu Gly Asp Trp Gly Leu Trp  
945 950 955 960

Leu Leu Ala Glu Gly Leu Gln His Pro Ala Cys Arg Leu Gln Lys Leu  
965 970 975

Trp Trp Leu Phe Gly Met Asp Leu Asn Lys Met Thr His Ser Arg Leu  
980 985 990

Ala Ala Leu Arg Val Thr Lys Pro Tyr Leu Asp Ile Gly Cys  
995 1000 1005

<210> 5  
<211> 3395  
<212> DNA  
<213> Homo sapiens

<400> 5  
attggtgagt ggggcagggc aggagggAAC tgaagagtGA gaaAGCATTa tttcagcaAA 60  
aggTCTTCC tccCTTGCTC actCCTCCAA ccACTGGCTC agCCTCTCCG cccgCTGCCT 120  
gtGAATGATG caATGGAAGG tGTGCTGGGG tcGCCtGTG tcccgtGcat aggAGCATCT 180  
cAGCCTCCAG gTCCTCTCCT ttGGGGCTTA CGGCACCCCCC atGCTACGAA CCAGCAGGCAg 240  
ggACGGCCTC tGTCGCTGT ccACCTACTT gGAAGAACTC gagGCTGTGG aactGAAGAA 300  
gttCAAGTTA tacCTGGGA CGCGACAGA gCTGGGAGAA ggCAAGATCC CCTGGGGAAg 360  
catGGAGAAG gCCGGTCCCC tggAAATGGC ccAGCTGCTC atCACCCACT tcGGGCCAGA 420  
ggAGGCGCTGG agGTTGGCTC tcAGCACCTT tgAGCGGATA AACAGGAAGG acCTGTGGGA 480  
gagAGGACAG agAGAGGACC tGGTGAAGGGA tacCCCACCT gGTGGCCCGT CCTCACTTGG 540  
gaaccAGTCA acATGCCTTC tggAAgtCTC tCTTGTCACT ccaAGAAAAG atCCCCAGGA 600  
aacCTACAGG gACTATGTCC gcAGGAAATT ccGGCTCATG gaAGACCGCA atGCGCGCCT 660

agggaaatgt	gtcaacctca	gccaccggta	cacccggctc	ctgctggtga	aggagcactc	720
aaaccccatg	caggtccagc	agcagcttct	ggacacaggc	cggggacacg	cgaggacagt	780
gggacaccag	gctagccccca	tcaagataga	gaccctttt	gagccagacg	aggagcgc	840
cgagccaccg	cgcaccgtgg	tcatgcaagg	cgcggcaggg	ataggcaagt	ccatgctggc	900
acacaagg	tgctggact	gggcggacgg	gaagctttc	caaggcagat	ttgattatct	960
cttctacatc	aactgcaggg	agatgaacca	gagtgccacg	aatgcagca	tgcaagac	1020
catcttcagc	tgctggcctg	agcccagcgc	gcctctccag	gagctcatcc	gagttcccga	1080
gcccctcctt	ttcatcatcg	acggcttcga	tgagctcaag	ccttcttcc	acgatcctca	1140
gggaccctgg	tgccctgtct	gggaggagaa	acggcccacg	gagctgttc	ttaacagctt	1200
aattcggaag	aagctgctcc	ctgagctatc	tttgctcatc	accacacggc	ccacggctt	1260
ggagaagctc	caccgtctgc	tggagcaccc	caggcatgtg	gagatcctgg	gcttctctga	1320
ggcagaaagg	aaggaatact	tctacaagta	tttccacaat	gcagagcagg	cgggccaagt	1380
cttcaattac	gtgagggaca	acgagcctct	cttcaccatg	tgcttcgtcc	ccctggtgt	1440
ctgggtggtg	tgtacctgcc	tccagcagca	gctggaggg	ggggggctgt	tgagacagac	1500
gtccaggacc	accactgcag	tgtacatgct	ctacctgctg	agtctgtatgc	aacccaagcc	1560
ggggcccccg	cgcctccagc	ccccacccaa	ccagagaggg	tttgctcct	tggcggcaga	1620
tgggctctgg	aatcagaaaa	tcctatttga	ggagcaggac	ctccggaagc	acggcctaga	1680
cgggaaagac	gtctctgcct	tcctcaacat	gaacatttc	cagaaggaca	tcaactgtga	1740
gaggtactac	agttcatcc	acttgagttt	ccaggaattc	tttgcagcta	tgtactatat	1800
cctggacgag	ggggagggcg	ggcaggccc	agaccaggac	gtgaccaggc	tgttgaccga	1860
gtacgcgttt	tctgaaagga	gttcctggc	actcaccagc	cgcttcctgt	ttggactcct	1920
gaacgaggag	accaggagcc	acctggagaa	gagtctctgc	tggaaggct	cgcgcacat	1980
caagatggac	ctgttgca	ggatccaaag	caaagctcag	agcgacggct	ccaccctgca	2040
gcagggctcc	ttggagttct	tca	gtacgcgtt	gtacgagatc	caggaggagg	2100
gcaggccctg	agccacttcc	aggtgtatgt	ggtcagcaac	attgcctcca	agatggagca	2160
catggtctcc	tcgttctgtc	tgaagcgctg	caggagcgcc	caggtgctgc	acttgtatgg	2220
cgcacccatc	agcgccggacg	gggaagacccg	cgcgaggtgc	tccgcaggag	cgcacacgct	2280
gttgggtgcag	ctcagaccag	agaggaccgt	tctgctggac	gcctacagt	aacatctggc	2340
agcggccctg	tgcaccaatc	caaaccgtat	agagctgtct	ctgtaccgaa	atgcctggg	2400
cagccgggggg	gtgaagctgc	tctgtcaagg	actcagacac	cccaactgca	aacttcagaa	2460
cctgaggctg	aagaggtgcc	gcatctccag	ctcagccgtc	gaggacctct	ctgcagctct	2520

catagccaat	aagaatttga	caaggatgga	tctcagtggc	aacggcggttgc	gattccagg	2580
catgatgctg	cttgcgagg	gcctgcggca	tccccagtc	aggctgcaga	tgattcagtt	2640
gaggaagtgt	cagctggagt	ccggggcttgc	tcaggagatg	gcttctgtgc	tcggcaccaa	2700
cccacatctg	gttgagttgg	acctgacagg	aaatgcactg	gaggatttgg	gcctgaggtt	2760
actatgccag	ggactgaggc	acccagtctg	cagactacgg	actttgtggc	tgtggctgga	2820
tagctgtggc	ctcacagcca	aggcttgc	aatcttac	ttcacccctgg	ggatcaacca	2880
gaccttgacc	gaccttacc	tgaccaacaa	cgccctaggg	gacacaggtg	tccgactgct	2940
ttgcaagcgg	ctgagccatc	ctggctgcaa	actccgagtc	ctctggttat	ttgggatgga	3000
cctgaataaa	atgacccaca	gtaggttggc	agcgcttcga	gtaacaaaac	cttatttgg	3060
cattggctgc	tgaatggtcc	tatctgctgg	ctctcccctg	agatctggac	agaggaagat	3120
gggaggggtgc	tcatcacccc	cccagcataa	tgatcagcct	ccttcctaga	gacagactca	3180
tgcagattga	gatcaaaaagt	ccctctgctt	gggatcaaata	taatgtttga	cagagctggc	3240
caggcgtggt	ggctcatgta	tgtaatccta	gcacttcgag	aggccgaggc	aggtggatca	3300
cgaggtcagg	agtttgagat	tagcctggcc	aagatggtga	aaccctgtct	ctactaaaaaa	3360
aaaaaaaaaa	ttagccagga	aaaaaaaaaa	aaaaaa			3395

<210> 6  
 <211> 950  
 <212> PRT  
 <213> Homo sapiens

<400> 6

Met	Leu	Arg	Thr	Ala	Gly	Arg	Asp	Gly	Leu	Cys	Arg	Leu	Ser	Thr	Tyr
1					5				10					15	

Leu	Glu	Glu	Leu	Glu	Ala	Val	Glu	Leu	Lys	Lys	Phe	Lys	Leu	Tyr	Leu
					20			25				30			

Gly	Thr	Ala	Thr	Glu	Leu	Gly	Glu	Gly	Lys	Ile	Pro	Trp	Gly	Ser	Met
					35			40				45			

Glu	Lys	Ala	Gly	Pro	Leu	Glu	Met	Ala	Gln	Leu	Leu	Ile	Thr	His	Phe
					50			55			60				

Gly	Pro	Glu	Glu	Ala	Trp	Arg	Leu	Ala	Leu	Ser	Thr	Phe	Glu	Arg	Ile
					65			70			75		80		

Asn	Arg	Lys	Asp	Leu	Trp	Glu	Arg	Gly	Gln	Arg	Glu	Asp	Leu	Val	Arg
					85			90				95			

Asp Thr Pro Pro Gly Gly Pro Ser Ser Leu Gly Asn Gln Ser Thr Cys  
100 105 110

Leu Leu Glu Val Ser Leu Val Thr Pro Arg Lys Asp Pro Gln Glu Thr  
115 120 125

Tyr Arg Asp Tyr Val Arg Arg Lys Phe Arg Leu Met Glu Asp Arg Asn  
130 135 140

Ala Arg Leu Gly Glu Cys Val Asn Leu Ser His Arg Tyr Thr Arg Leu  
145 150 155 160

Leu Leu Val Lys Glu His Ser Asn Pro Met Gln Val Gln Gln Gln Leu  
165 170 175

Leu Asp Thr Gly Arg Gly His Ala Arg Thr Val Gly His Gln Ala Ser  
180 185 190

Pro Ile Lys Ile Glu Thr Leu Phe Glu Pro Asp Glu Glu Arg Pro Glu  
195 200 205

Pro Pro Arg Thr Val Val Met Gln Gly Ala Ala Gly Ile Gly Lys Ser  
210 215 220

Met Leu Ala His Lys Val Met Leu Asp Trp Ala Asp Gly Lys Leu Phe  
225 230 235 240

Gln Gly Arg Phe Asp Tyr Leu Phe Tyr Ile Asn Cys Arg Glu Met Asn  
245 250 255

Gln Ser Ala Thr Glu Cys Ser Met Gln Asp Leu Ile Phe Ser Cys Trp  
260 265 270

Pro Glu Pro Ser Ala Pro Leu Gln Glu Leu Ile Arg Val Pro Glu Arg  
275 280 285

Leu Leu Phe Ile Ile Asp Gly Phe Asp Glu Leu Lys Pro Ser Phe His  
290 295 300

Asp Pro Gln Gly Pro Trp Cys Leu Cys Trp Glu Glu Lys Arg Pro Thr  
305 310 315 320

Glu Leu Leu Leu Asn Ser Leu Ile Arg Lys Lys Leu Leu Pro Glu Leu  
325 330 335

Ser Leu Leu Ile Thr Thr Arg Pro Thr Ala Leu Glu Lys Leu His Arg  
340 345 350

Leu Leu Glu His Pro Arg His Val Glu Ile Leu Gly Phe Ser Glu Ala  
355 360 365

Glu Arg Lys Glu Tyr Phe Tyr Lys Tyr Phe His Asn Ala Glu Gln Ala  
370 375 380

Gly Gln Val Phe Asn Tyr Val Arg Asp Asn Glu Pro Leu Phe Thr Met  
385 390 395 400

Cys Phe Val Pro Leu Val Cys Trp Val Val Cys Thr Cys Leu Gln Gln  
405 410 415

Gln Leu Glu Gly Gly Leu Leu Arg Gln Thr Ser Arg Thr Thr Thr  
420 425 430

Ala Val Tyr Met Leu Tyr Leu Leu Ser Leu Met Gln Pro Lys Pro Gly  
435 440 445

Ala Pro Arg Leu Gln Pro Pro Pro Asn Gln Arg Gly Leu Cys Ser Leu  
450 455 460

Ala Ala Asp Gly Leu Trp Asn Gln Lys Ile Leu Phe Glu Glu Gln Asp  
465 470 475 480

Leu Arg Lys His Gly Leu Asp Gly Glu Asp Val Ser Ala Phe Leu Asn  
485 490 495

Met Asn Ile Phe Gln Lys Asp Ile Asn Cys Glu Arg Tyr Tyr Ser Phe  
500 505 510

Ile His Leu Ser Phe Gln Glu Phe Phe Ala Ala Met Tyr Tyr Ile Leu  
515 520 525

Asp Glu Gly Glu Gly Ala Gly Pro Asp Gln Asp Val Thr Arg Leu  
530 535 540

Leu Thr Glu Tyr Ala Phe Ser Glu Arg Ser Phe Leu Ala Leu Thr Ser  
545 550 555 560

Arg Phe Leu Phe Gly Leu Leu Asn Glu Glu Thr Arg Ser His Leu Glu  
565 570 575

Lys Ser Leu Cys Trp Lys Val Ser Pro His Ile Lys Met Asp Leu Leu  
580 585 590

Gln Trp Ile Gln Ser Lys Ala Gln Ser Asp Gly Ser Thr Leu Gln Gln  
595 600 605

Gly Ser Leu Glu Phe Phe Ser Cys Leu Tyr Glu Ile Gln Glu Glu Glu  
610 615 620

Phe Ile Gln Gln Ala Leu Ser His Phe Gln Val Ile Val Val Ser Asn  
625 630 635 640

Ile Ala Ser Lys Met Glu His Met Val Ser Ser Phe Cys Leu Lys Arg  
645 650 655

Cys Arg Ser Ala Gln Val Leu His Leu Tyr Gly Ala Thr Tyr Ser Ala  
660 665 670

Asp Gly Glu Asp Arg Ala Arg Cys Ser Ala Gly Ala His Thr Leu Leu  
675 680 685

Val Gln Leu Arg Pro Glu Arg Thr Val Leu Leu Asp Ala Tyr Ser Glu  
690 695 700

His Leu Ala Ala Ala Leu Cys Thr Asn Pro Asn Leu Ile Glu Leu Ser  
705 710 715 720

Leu Tyr Arg Asn Ala Leu Gly Ser Arg Gly Val Lys Leu Leu Cys Gln  
725 730 735

Gly Leu Arg His Pro Asn Cys Lys Leu Gln Asn Leu Arg Leu Lys Arg  
740 745 750

Cys Arg Ile Ser Ser Ala Cys Glu Asp Leu Ser Ala Ala Leu Ile.  
755 760 765

Ala Asn Lys Asn Leu Thr Arg Met Asp Leu Ser Gly Asn Gly Val Gly  
770 775 780

Phe Pro Gly Met Met Leu Leu Cys Glu Gly Leu Arg His Pro Gln Cys  
785 790 795 800

Arg Leu Gln Met Ile Gln Leu Arg Lys Cys Gln Leu Glu Ser Gly Ala  
805 810 815

Cys Gln Glu Met Ala Ser Val Leu Gly Thr Asn Pro His Leu Val Glu

820

825

830

Leu Asp Leu Thr Gly Asn Ala Leu Glu Asp Leu Gly Leu Arg Leu Leu  
835 840 845

Cys Gln Gly Leu Arg His Pro Val Cys Arg Leu Arg Thr Leu Trp Leu  
850 855 860

Trp Leu Asp Ser Cys Gly Leu Thr Ala Lys Ala Cys Glu Asn Leu Tyr  
865 870 875 880

Phe Thr Leu Gly Ile Asn Gln Thr Leu Thr Asp Leu Tyr Leu Thr Asn  
885 890 895

Asn Ala Leu Gly Asp Thr Gly Val Arg Leu Leu Cys Lys Arg Leu Ser  
900 905 910

His Pro Gly Cys Lys Leu Arg Val Leu Trp Leu Phe Gly Met Asp Leu  
915 920 925

Asn Lys Met Thr His Ser Arg Leu Ala Ala Leu Arg Val Thr Lys Pro  
930 935 940

Tyr Leu Asp Ile Gly Cys  
945 950

<210> 7  
<211> 3221  
<212> DNA  
<213> Homo sapiens

<400> 7  
atgggtgagt ggggcagggc aggagggAAC tgaagagtGA gaaAGCATTa tttcAGCAAA 60  
aggTCTTCC TCCCTTGCTC ACTCCTCCAA CCACTGGCTC AGCCTCTCCG CCCGCTGCCT 120  
gtGAATGATG CAATGGAAGG TGTGCTGGGG TCGCCCTGTG TCCCCTGTCAT AGGAGCATCT 180  
cAGCCTCCAG GTCCTCTCCT TTGGGGCTTA CGGCACCCCCC ATGCTACGAA CGCAGGGCAG 240  
GGACGGCCTC TGTCGCTGT CCACCTACTT GGAAGAACTC GAGGCTGTGG AACtGAAGAA 300  
GTTCAAGTTA TACCTGGGG A CGCGACAGA GCTGGGAGAA GGCAAGATCC CCTGGGGAAAG 360  
CATGGAGAAG GCCGGTCCCC TGGAAATGGC CCAGCTGCTC ATCACCCACT TCAGGGCCAGA 420  
GGAGGCCTGG AGGTTGGCTC TCAgCACCTT TGAGCGATA AACAGGAAGG ACCTGTGGGA 480  
GAGAGGACAG AGAGAGGACC TGGTGGGG A TACCCACCT GGTGGCCCGT CCTCACTTGG 540  
GAACCAGTCA ACATGCCTTC TGGAAgTCTC TCTTGTCACT CCAAGAAAAG ATCCCCAGGA 600

aacctacagg	gactatgtcc	gcagggaaatt	ccggctcatg	gaagaccgca	atgcgcgcct	660
aggggaatgt	gtcaacctca	gccaccggta	cacccggctc	ctgctggtga	aggagcactc	720
aaaccccatg	caggtccagc	agcagttct	ggacacagggc	cggggacacg	cgaggaccgt	780
gggacaccag	gctagccccca	tcaagataga	gaccctctt	gagccagacg	aggagcgccc	840
cgagccacccg	cgcaccgtgg	tcatgcaagg	cgcggcaggg	ataggcaagt	ccatgctggc	900
acacaaggtg	atgctggact	gggcggacgg	gaagcttttc	caaggcagat	ttgattatct	960
cttctacatc	aactgcaggg	agatgaacca	gagtgccacg	aatgcagca	tgcaagacct	1020
catcttcagc	tgctggcctg	agcccagcgc	gcctctccag	gagctcatcc	gagttcccga	1080
gcccctcctt	ttcatcatcg	acggcttcga	tgagctcaag	ccttcttcc	acgatcctca	1140
gggaccctgg	tgcctctgct	gggaggagaa	acggcccacg	gagctgttc	ttaacagctt	1200
aattcggaaag	aagctgctcc	ctgagctatc	tttgcatac	accacacggc	ccacggcttt	1260
ggagaagctc	caccgtctgc	tggagcaccc	caggcatgtg	gagatcctgg	gcttctctga	1320
ggcagaaaagg	aaggaatact	tctacaagta	tttccacaat	gcagagcagg	cgggccaagt	1380
cttcaattac	gtgagggaca	acgagcctct	cttcaccatg	tgcttcgtcc	ccctggtgtg	1440
ctgggtggtg	tgtacctgcc	tccagcagca	gctggaggg	ggggggctgt	tgagacagac	1500
gtccaggacc	accactgcag	tgtacatgct	ctacctgtg	agtctgatgc	aacccaagcc	1560
ggggggcccg	cgcctccagc	ccccacccaa	ccagagaggg	ttgtgctcct	tggcggcaga	1620
tgggctctgg	aatcagaaaa	tcctatttga	ggagcaggac	ctccggaagc	acggcctaga	1680
cgggaaagac	gtctctgcct	tcctcaacat	gaacatcttc	cagaaggaca	tcaactgtga	1740
gaggtactac	agttcatcc	acttgagttt	ccaggaattc	tttgcagcta	tgtactatat	1800
cctggacgag	ggggagggcg	gggcaggccc	agaccaggac	gtgaccaggg	tgttggaccga	1860
gtacgcgttt	tctgaaagga	gcttcctggc	actcaccagc	cgcttcctgt	ttggactcct	1920
gaacgaggag	accaggagcc	acctggagaa	gagtctctgc	tggaagggtct	cggccacat	1980
caagatggac	ctgttgcagt	ggatccaaag	caaagctcag	agcgacggct	ccaccctgca	2040
gcagggctcc	ttggagttct	ttagctgctt	gtacgagatc	caggaggagg	agtttatcca	2100
gcaggccctg	agccacttcc	aggtgatcgt	ggtcagcaac	attgcctcca	agatggagca	2160
catggcttcc	tcgttctgtc	tgaagcgctg	caggagcgcc	caggtgctgc	acttgtatgg	2220
cgcacccatc	agcgcggacg	gggaagacccg	cgcgaggtgc	tccgcaggag	cgcacacgct	2280
gttgggtcag	ctcagaccag	agaggaccgt	tctgctggac	gcctacagtg	aacatctggc	2340
agcggccctg	tgcaccaatc	caaacctgat	agagctgtct	ctgtaccgaa	atgcctggg	2400
cagccgggggg	gtgaagctgc	tctgtcaagg	actcagacac	cccaactgca	aacttcagaa	2460

cctgaggcgt	aagaggtgcc	gcatctccag	ctcagcctgc	gaggacctct	ctgcagctct	2520
catagccaat	aagaatttga	caaggatgga	tctcagtggc	aacggcggttg	gattcccagg	2580
catgatgctg	ctttgcgagg	gcctgceggca	tccccagtgc	aggctgcaga	tgattcagtt	2640
gaggaagtgt	cagctggagt	ccggggcttg	tcaggagatg	gcttctgtgc	tcggcaccaa	2700
cccacatctg	gttgagttgg	acctgacagg	aaatgcactg	gaggatttgg	gcctgagggtt	2760
actatgccag	ggactgaggc	accaggctcg	cagactacgg	actttgtggt	ggttatttgg	2820
gatggacctg	aataaaatga	cccacagtag	gttggcagcg	cttcgagtaa	caaaacctta	2880
tttggacatt	ggctgctgaa	ttgtcctatc	tgctggctct	cccctgagat	ctggacagag	2940
gaagatggga	gggtgctcat	cacccccc	gcataatgt	cagcctcctt	cctagagaca	3000
gactcatgca	gattgagatc	aaaagtccct	ctgcttggga	tcaaattaat	gtttgacaga	3060
gctggccagg	cgtggtggt	catgtatgta	atcctagcac	ttcgagaggc	cgaggcaggt	3120
ggatcacgag	gtcaggagtt	tgagattagc	ctggccaaga	tggtaaaacc	ctgtctctac	3180
taaaaaataaa	aaaaaattag	ccagaaaaaa	aaaaaaaaaa	a		3221

<210> 8  
 <211> 892  
 <212> PRT  
 <213> Homo sapiens

<400> 8

Met	Leu	Arg	Thr	Ala	Gly	Arg	Asp	Gly	Leu	Cys	Arg	Leu	Ser	Thr	Tyr
1									5		10				15

Leu	Glu	Glu	Leu	Glu	Ala	Val	Glu	Leu	Lys	Lys	Phe	Lys	Leu	Tyr	Leu
								20		25				30	

Gly	Thr	Ala	Thr	Glu	Leu	Gly	Glu	Gly	Lys	Ile	Pro	Trp	Gly	Ser	Met
								35		40				45	

Glu	Lys	Ala	Gly	Pro	Leu	Glu	Met	Ala	Gln	Leu	Leu	Ile	Thr	His	Phe
							50		55				60		

Gly	Pro	Glu	Glu	Ala	Trp	Arg	Leu	Ala	Leu	Ser	Thr	Phe	Glu	Arg	Ile
							65		70				75		80

Asn	Arg	Lys	Asp	Leu	Trp	Glu	Arg	Gly	Gln	Arg	Glu	Asp	Leu	Val	Arg
								85		90				95	

Asp	Thr	Pro	Pro	Gly	Gly	Pro	Ser	Ser	Leu	Gly	Asn	Gln	Ser	Thr	Cys
								100		105				110	

Leu Leu Glu Val Ser Leu Val Thr Pro Arg Lys Asp Pro Gln Glu Thr  
115 120 125

Tyr Arg Asp Tyr Val Arg Arg Lys Phe Arg Leu Met Glu Asp Arg Asn  
130 135 140

Ala Arg Leu Gly Glu Cys Val Asn Leu Ser His Arg Tyr Thr Arg Leu  
145 150 155 160

Leu Leu Val Lys Glu His Ser Asn Pro Met Gln Val Gln Gln Gln Leu  
165 170 175

Leu Asp Thr Gly Arg Gly His Ala Arg Thr Val Gly His Gln Ala Ser  
180 185 190

Pro Ile Lys Ile Glu Thr Leu Phe Glu Pro Asp Glu Glu Arg Pro Glu  
195 200 205

Pro Pro Arg Thr Val Val Met Gln Gly Ala Ala Gly Ile Gly Lys Ser  
210 215 220

Met Leu Ala His Lys Val Met Leu Asp Trp Ala Asp Gly Lys Leu Phe  
225 230 235 240

Gln Gly Arg Phe Asp Tyr Leu Phe Tyr Ile Asn Cys Arg Glu Met Asn  
245 250 255

Gln Ser Ala Thr Glu Cys Ser Met Gln Asp Leu Ile Phe Ser Cys Trp  
260 265 270

Pro Glu Pro Ser Ala Pro Leu Gln Glu Leu Ile Arg Val Pro Glu Arg  
275 280 285

Leu Leu Phe Ile Ile Asp Gly Phe Asp Glu Leu Lys Pro Ser Phe His  
290 295 300

Asp Pro Gln Gly Pro Trp Cys Leu Cys Trp Glu Glu Lys Arg Pro Thr  
305 310 315 320

Glu Leu Leu Leu Asn Ser Leu Ile Arg Lys Lys Leu Leu Pro Glu Leu  
325 330 335

Ser Leu Leu Ile Thr Thr Arg Pro Thr Ala Leu Glu Lys Leu His Arg  
340 345 350

Leu Leu Glu His Pro Arg His Val Glu Ile Leu Gly Phe Ser Glu Ala  
355 360 365

Glu Arg Lys Glu Tyr Phe Tyr Lys Tyr Phe His Asn Ala Glu Gln Ala  
370 375 380

Gly Gln Val Phe Asn Tyr Val Arg Asp Asn Glu Pro Leu Phe Thr Met  
385 390 395 400

Cys Phe Val Pro Leu Val Cys Trp Val Val Cys Thr Cys Leu Gln Gln  
405 410 415

Gln Leu Glu Gly Gly Leu Leu Arg Gln Thr Ser Arg Thr Thr Thr  
420 425 430

Ala Val Tyr Met Leu Tyr Leu Leu Ser Leu Met Gln Pro Lys Pro Gly  
435 440 445

Ala Pro Arg Leu Gln Pro Pro Pro Asn Gln Arg Gly Leu Cys Ser Leu  
450 455 460

Ala Ala Asp Gly Leu Trp Asn Gln Lys Ile Leu Phe Glu Glu Gln Asp  
465 470 475 480

Leu Arg Lys His Gly Leu Asp Gly Glu Asp Val Ser Ala Phe Leu Asn  
485 490 495

Met Asn Ile Phe Gln Lys Asp Ile Asn Cys Glu Arg Tyr Tyr Ser Phe  
500 505 510

Ile His Leu Ser Phe Gln Glu Phe Phe Ala Ala Met Tyr Tyr Ile Leu  
515 520 525

Asp Glu Gly Glu Gly Ala Gly Pro Asp Gln Asp Val Thr Arg Leu  
530 535 540

Leu Thr Glu Tyr Ala Phe Ser Glu Arg Ser Phe Leu Ala Leu Thr Ser  
545 550 555 560

Arg Phe Leu Phe Gly Leu Leu Asn Glu Glu Thr Arg Ser His Leu Glu  
565 570 575

Lys Ser Leu Cys Trp Lys Val Ser Pro His Ile Lys Met Asp Leu Leu  
580 585 590

Gln Trp Ile Gln Ser Lys Ala Gln Ser Asp Gly Ser Thr Leu Gln Gln  
595 600 605

Gly Ser Leu Glu Phe Phe Ser Cys Leu Tyr Glu Ile Gln Glu Glu Glu  
610 615 620

Phe Ile Gln Gln Ala Leu Ser His Phe Gln Val Ile Val Val Ser Asn  
625 630 635 640

Ile Ala Ser Lys Met Glu His Met Val Ser Ser Phe Cys Leu Lys Arg  
645 650 655

Cys Arg Ser Ala Gln Val Leu His Leu Tyr Gly Ala Thr Tyr Ser Ala  
660 665 670

Asp Gly Glu Asp Arg Ala Arg Cys Ser Ala Gly Ala His Thr Leu Leu  
675 680 685

Val Gln Leu Arg Pro Glu Arg Thr Val Leu Leu Asp Ala Tyr Ser Glu  
690 695 700

His Leu Ala Ala Ala Leu Cys Thr Asn Pro Asn Leu Ile Glu Leu Ser  
705 710 715 720

Leu Tyr Arg Asn Ala Leu Gly Ser Arg Gly Val Lys Leu Leu Cys Gln  
725 730 735

Gly Leu Arg His Pro Asn Cys Lys Leu Gln Asn Leu Arg Leu Lys Arg  
740 745 750

Cys Arg Ile Ser Ser Ala Cys Glu Asp Leu Ser Ala Ala Leu Ile  
755 760 765

Ala Asn Lys Asn Leu Thr Arg Met Asp Leu Ser Gly Asn Gly Val Gly  
770 775 780

Phe Pro Gly Met Met Leu Leu Cys Glu Gly Leu Arg His Pro Gln Cys  
785 790 795 800

Arg Leu Gln Met Ile Gln Leu Arg Lys Cys Gln Leu Glu Ser Gly Ala  
805 810 815

Cys Gln Glu Met Ala Ser Val Leu Gly Thr Asn Pro His Leu Val Glu  
820 825 830

Leu Asp Leu Thr Gly Asn Ala Leu Glu Asp Leu Gly Leu Arg Leu Leu

835

840

845

Cys Gln Gly Leu Arg His Pro Val Cys Arg Leu Arg Thr Leu Trp Trp  
 850                    855                    860

Leu Phe Gly Met Asp Leu Asn Lys Met Thr His Ser Arg Leu Ala Ala  
 865                    870                    875                    880

Leu Arg Val Thr Lys Pro Tyr Leu Asp Ile Gly Cys  
 885                    890

<210> 9  
<211> 3102  
<212> DNA  
<213> Mus musculus

<400> 9	
atgttgcgt ctacagccag gnatggcctc tatcgactgt ctacacctt ggaagaactc	60
gaggctgggg aactgaagaa attcaaattt ttcctggga ttgcagagga cctgagccag	120
gacaaaattt cctggggacg aatggagaag gctggtcctc tggaaatggc tcagctgtat	180
gtggcccaaca tggggacaag ggaggcttgg cttctggctc tcagcacctt tcagaggatt	240
cacaggaagg acctgtggga gcgaggacag ggagaagacc tggtaggggg taaggagggc	300
aaggggatc tacagacaac ctacaaagac tatgtccgaa ggaaattcca gctaattggaa	360
gaccgcaatg cacgattagg cgaatgtgtt aacctgagca atcgttacac tcggcttctc	420
ctagtaaaag aacactcaaa tcctatctgg acacagcaga aattttaga tgttagagtgg	480
gaacgctcca gaaccaggcg tcaccagact agtcctatcc aaatggagac cctcttttag	540
ccagacgaag aacgccccga gccaccacac acagtggat tacaaggggc agcggggatg	600
gggaagtcca tgctggccca caaagtgtatg ttggactggg ccgatggag gctcttccaa	660
ggccggtttg attatgtctt ctatatcagc tgcagggagt tgaatagaag ccacacccag	720
tgcagtgtac aagacctcat ctccagctgc tggccggagc gtggatatac cctcgaagac	780
ctcatgcagg ctccctgaccg tctcttattt atcattgtatg gcttcgataa actccatcct	840
tcttccatg atgctcaggg tccctggcgc ctctgtggg aggagaaaca acctactgaa	900
gtcctcctcg gaagtctgat tcggagggtt cttctgcccc aggtctctct gctcatcacc	960
acacgaccct gtgcactgga gaagctgcac ggcttgctag aacacccag gcacgtggag	1020
atcctgggct tctccgagga agcttaggaag gaatatttct acagatattt ccacaacact	1080
ggacaagcaa gccgggtgtt aagcttcttgc atggactatg agccccccttt taccatgtgt	1140
tttgttccca tggtgtcctg ggtggctgc acctgcctaa agcagcagct ggaaagtggg	1200

gagctttaa gacaaacacc taggaccacc acagctgtt atatgttcta ccttctgagc	1260
ctgatgcagc ccaagccagg gactccaacc ttcaaagtcc cagccaaacca gagaggcctg	1320
gtctctctgg ctgcagaggg cctctggaat cagaagattc tatttgatga acaggatctt	1380
gggaaacacg gcctagatgg agcagatgtg tccacttcc tcaacgtgaa catattccag	1440
aagggtatca aatgtgagaa attctacagc ttcatccacc tgagttcca ggaattcttc	1500
gcagccatgt actgtgcact gaatggcaga gaggcggtga ggagagcgct ggctgagtat	1560
ggttttcgg aaaggaacctt cttggccctc acggtccact ttctgtttgg cctcctcaac	1620
gaagagatga gatgctacct tgagaggaat ctggctgga gcatctcccc tcaggtgaag	1680
gaggaagtgt tggcatggat ccaaaacaag gctggagtg aaggctccac cctgcagcat	1740
ggctccctgg agctactcag ctgcttgtat gaggtccagg aggaggactt catccagcag	1800
gccctgagcc actttcaagt ggtttagtc agaagcatct caacaaagat ggagcacatg	1860
gtctgctcgt tttgtgcgag gtattgcaga agtacagaag tgcttcactt gcatggaggt	1920
gcttatagta caggcatgga ggacgaccca ccagaacctt caggagtcca gactcagtcc	1980
acataacttac aggaaaggaa catgctgcct gatgtctaca gtgcataacct ttcagcagct	2040
gtctgtacca actccaacct gatcgagctg gccttataacc gaaatgcctt gggcagccag	2100
ggtgtaaggc tgctctgtca aggccctcga catgccagct gcaagctgca gaacctgagg	2160
ctgaagaggt gtcagatctc cggatcagcc tgccaggacc tcgcagccgc tgtcatcgcc	2220
aacaggaatt taatcaggct ggacctcagt gacaacagca ttggggtgcc aggccctggag	2280
ctgctctgtg aggggctgca gcaccccagg tgtaggctgc agatgatcca gctgaggaag	2340
tgtctgttgg aggctgcagc tggccgatcc ctggcttctg ttctcagcaa caactcatat	2400
ctggtagaac tggatctgac aggaaacccc ttggaagatt cggggctgaa gttactgtgt	2460
caagggctaa ggcacctgt ctgcaggctg cgtaccctgt ggctgaagat ctgccacctt	2520
ggacaagctt cctgcgaaga tctggctct actctaaaa tgaaccagag cctgctggag	2580
ctggacctgg gtctgaatga tcttgagat tctggggtgc ttctgctgtg tgaaggcctc	2640
agtcatccag attgcaaact ccagaccctt cggttggca tttgccact gggctcagtc	2700
gcgtgtgtgg ggatgcctcag tgtgctccag gtcaacacat gcctccaaga gctggacctg	2760
agcttcaatg acttgggaga cagggccctg cagctgctgg gggaaaggcct gaggcaccag	2820
acctgcagac tccagaagct gtggctggac aactgcggac tcacctccaa agcatgtgag	2880
gacctttctt ctatcctggg aatcagccag accctgcatt agctttattt gaccaataat	2940
gctctggggg acacaggtgt ctgtctgctg tgcaagaggc tgaggcatcc aggctgcaag	3000
cttcgagtcc tggatggac ctgaataaaa agactcacag gaggatggca	3060

gcacttcgag tcacaaaacc gtacctggat attgggtgtt ga

3102

<210> 10  
<211> 1033  
<212> PRT  
<213> Mus musculus  
  
<400> 10

Met Leu Pro Ser Thr Ala Arg Asp Gly Leu Tyr Arg Leu Ser Thr Tyr  
1 5 10 15

Leu Glu Glu Leu Glu Ala Gly Glu Leu Lys Lys Phe Lys Leu Phe Leu  
20 25 30

Gly Ile Ala Glu Asp Leu Ser Gln Asp Lys Ile Pro Trp Gly Arg Met  
35 40 45

Glu Lys Ala Gly Pro Leu Glu Met Ala Gln Leu Met Val Ala His Met  
50 55 60

Gly Thr Arg Glu Ala Trp Leu Leu Ala Leu Ser Thr Phe Gln Arg Ile  
65 70 75 80

His Arg Lys Asp Leu Trp Glu Arg Gly Gln Gly Glu Asp Leu Val Arg  
85 90 95

Gly Lys Glu Gly Lys Gly Asp Leu Gln Thr Thr Tyr Lys Asp Tyr Val  
100 105 110

Arg Arg Lys Phe Gln Leu Met Glu Asp Arg Asn Ala Arg Leu Gly Glu  
115 120 125

Cys Val Asn Leu Ser Asn Arg Tyr Thr Arg Leu Leu Leu Val Lys Glu  
130 135 140

His Ser Asn Pro Ile Trp Thr Gln Gln Lys Phe Val Asp Val Glu Trp  
145 150 155 160

Glu Arg Ser Arg Thr Arg Arg His Gln Thr Ser Pro Ile Gln Met Glu  
165 170 175

Thr Leu Phe Glu Pro Asp Glu Glu Arg Pro Glu Pro Pro His Thr Val  
180 185 190

Val Leu Gln Gly Ala Ala Gly Met Gly Lys Ser Met Leu Ala His Lys  
195 200 205

Val Met Leu Asp Trp Ala Asp Gly Arg Leu Phe Gln Gly Arg Phe Asp  
210 215 220

Tyr Val Phe Tyr Ile Ser Cys Arg Glu Leu Asn Arg Ser His Thr Gln  
225 230 235 240

Cys Ser Val Gln Asp Leu Ile Ser Ser Cys Trp Pro Glu Arg Gly Ile  
245 250 255

Ser Leu Glu Asp Leu Met Gln Ala Pro Asp Arg Leu Leu Phe Ile Ile  
260 265 270

Asp Gly Phe Asp Lys Leu His Pro Ser Phe His Asp Ala Gln Gly Pro  
275 280 285

Trp Cys Leu Cys Trp Glu Glu Lys Gln Pro Thr Glu Val Leu Leu Gly  
290 295 300

Ser Leu Ile Arg Arg Leu Leu Leu Pro Gln Val Ser Leu Leu Ile Thr  
305 310 315 320

Thr Arg Pro Cys Ala Leu Glu Lys Leu His Gly Leu Leu Glu His Pro  
325 330 335

Arg His Val Glu Ile Leu Gly Phe Ser Glu Glu Ala Arg Lys Glu Tyr  
340 345 350

Phe Tyr Arg Tyr Phe His Asn Thr Gly Gln Ala Ser Arg Val Leu Ser  
355 360 365

Phe Leu Met Asp Tyr Glu Pro Leu Phe Thr Met Cys Phe Val Pro Met  
370 375 380

Val Ser Trp Val Val Cys Thr Cys Leu Lys Gln Gln Leu Glu Ser Gly  
385 390 395 400

Glu Leu Leu Arg Gln Thr Pro Arg Thr Thr Thr Ala Val Tyr Met Phe  
405 410 415

Tyr Leu Leu Ser Leu Met Gln Pro Lys Pro Gly Thr Pro Thr Phe Lys  
420 425 430

Val Pro Ala Asn Gln Arg Gly Leu Val Ser Leu Ala Ala Glu Gly Leu  
435 440 445

Trp Asn Gln Lys Ile Leu Phe Asp Glu Gln Asp Leu Gly Lys His Gly  
450 455 460

Leu Asp Gly Ala Asp Val Ser Thr Phe Leu Asn Val Asn Ile Phe Gln  
465 470 475 480

Lys Gly Ile Lys Cys Glu Lys Phe Tyr Ser Phe Ile His Leu Ser Phe  
485 490 495

Gln Glu Phe Phe Ala Ala Met Tyr Cys Ala Leu Asn Gly Arg Glu Ala  
500 505 510

Val Arg Arg Ala Leu Ala Glu Tyr Gly Phe Ser Glu Arg Asn Phe Leu  
515 520 525

Ala Leu Thr Val His Phe Leu Phe Gly Leu Leu Asn Glu Glu Met Arg  
530 535 540

Cys Tyr Leu Glu Arg Asn Leu Gly Trp Ser Ile Ser Pro Gln Val Lys  
545 550 555 560

Glu Glu Val Leu Ala Trp Ile Gln Asn Lys Ala Gly Ser Glu Gly Ser  
565 570 575

Thr Leu Gln His Gly Ser Leu Glu Leu Leu Ser Cys Leu Tyr Glu Val  
580 585 590

Gln Glu Glu Asp Phe Ile Gln Gln Ala Leu Ser His Phe Gln Val Val  
595 600 .. 605

Val Val Arg Ser Ile Ser Thr Lys Met Glu His Met Val Cys Ser Phe  
610 615 620

Cys Ala Arg Tyr Cys Arg Ser Thr Glu Val Leu His Leu His Gly Ser  
625 630 635 640

Ala Tyr Ser Thr Gly Met Glu Asp Asp Pro Pro Glu Pro Ser Gly Val  
645 650 655

Gln Thr Gln Ser Thr Tyr Leu Gln Glu Arg Asn Met Leu Pro Asp Val  
660 665 670

Tyr Ser Ala Tyr Leu Ser Ala Ala Val Cys Thr Asn Ser Asn Leu Ile  
675 680 685

Glu Leu Ala Leu Tyr Arg Asn Ala Leu Gly Ser Gln Gly Val Arg Leu  
690 695 700

Leu Cys Gln Gly Leu Arg His Ala Ser Cys Lys Leu Gln Asn Leu Arg  
705 710 715 720

Leu Lys Arg Cys Gln Ile Ser Gly Ser Ala Cys Gln Asp Leu Ala Ala  
725 730 735

Ala Val Ile Ala Asn Arg Asn Leu Ile Arg Leu Asp Leu Ser Asp Asn  
740 745 750

Ser Ile Gly Val Pro Gly Leu Glu Leu Leu Cys Glu Gly Leu Gln His  
755 760 765

Pro Arg Cys Arg Leu Gln Met Ile Gln Leu Arg Lys Cys Leu Leu Glu  
770 775 780

Ala Ala Ala Gly Arg Ser Leu Ala Ser Val Leu Ser Asn Asn Ser Tyr  
785 790 795 800

Leu Val Glu Leu Asp Leu Thr Gly Asn Pro Leu Glu Asp Ser Gly Leu  
805 810 815

Lys Leu Leu Cys Gln Gly Leu Arg His Pro Val Cys Arg Leu Arg Thr  
820 825 830

Leu Trp Leu Lys Ile Cys His Leu Gly Gln Ala Ser Cys Glu Asp Leu  
835 840 845

Ala Ser Thr Leu Lys Met Asn Gln Ser Leu Leu Glu Leu Asp Leu Gly  
850 855 860

Leu Asn Asp Leu Gly Asp Ser Gly Val Leu Leu Leu Cys Glu Gly Leu  
865 870 875 880

Ser His Pro Asp Cys Lys Leu Gln Thr Leu Arg Leu Gly Ile Cys Arg  
885 890 895

Leu Gly Ser Val Ala Cys Val Gly Ile Ala Ser Val Leu Gln Val Asn  
900 905 910

Thr Cys Leu Gln Glu Leu Asp Leu Ser Phe Asn Asp Leu Gly Asp Arg  
915 920 925

Gly Leu Gln Leu Leu Gly Glu Gly Leu Arg His Gln Thr Cys Arg Leu

930

935

940

Gln Lys Leu Trp Leu Asp Asn Cys Gly Leu Thr Ser Lys Ala Cys Glu  
 945                    950                    955                    960

Asp Leu Ser Ser Ile Leu Gly Ile Ser Gln Thr Leu His Glu Leu Tyr  
 965                    970                    975

Leu Thr Asn Asn Ala Leu Gly Asp Thr Gly Val Cys Leu Leu Cys Lys  
 980                    985                    990

Arg Leu Arg His Pro Gly Cys Lys Leu Arg Val Leu Trp Leu Phe Gly  
 995                    1000                    1005

Met Asp Leu Asn Lys Lys Thr His Arg Arg Met Ala Ala Leu Arg  
 1010                    1015                    1020

Val Thr Lys Pro Tyr Leu Asp Ile Gly Cys  
 1025                    1030

<210> 11  
<211> 3039  
<212> DNA  
<213> Homo sapiens

<400> 11	
atggcagatt catcatcatc ttctttcttt cctgatttg ggctgctatt gtatttggag	60
gagctaaaca aagaggaatt aaatacattc aagttattcc taaaggagac catggaacct	120
gagcatggcc tgacaccctg gaatgaagtg aagaaggcca ggcgggagga cctggccaat	180
ttgatgaaga aatatttatcc aggagagaaa gcctggagtg tgtctctcaa aatctttggc	240
aagatgaacc tgaaggatct gtgtgagaga gcgaaagaag agatcaactg gtcggcccaag	300
actataggac cagatgatgc caaggctgga gagacacaag aagatcagga ggcagtgctg	360
ggtgatggaa cagaatacag aaatagaata aaggaaaaat tttgcatcac ttgggacaag	420
aagtctttgg ctggaaagcc tgaagatttc catcatggaa ttgcagagaa agatagaaaa	480
ctgttggAAC acttgttgcgatgtc aaaaccggtg cacagccaca gatcggttg	540
cttcaggagatgtc tgggaaaaca accttggatgtca gaaaggcaat gtttagattgg	600
gcagagggca gtctctacca gcagagggtt aagtatgttt tttatctcaa tgggagagaa	660
attaaccagc tgaaagagag aagctttgct caattgatat caaaggactg gcccagcaca	720
gaaggccccca ttgaagaaaat catgtaccag ccaagttagcc tcttggatgtt tattgacagt	780
ttcgatgaac tgaactttgc ctttgaagaa cctgagtttg cactgtgcga agactggacc	840

caagaacacc cagtgtcctt cctcatgagt agtttgctga ggaaagtgtat gtcgcctgag 900  
 gcatcccttat tggtgacaac aagactcaca acttctaaga gactaaagca gttgttgaag 960  
 aatcaccatt atgttagagct actaggaatg tctgaggatg caagagagga gtatatttac 1020  
 cagtttttg aagataagag gtgggccatg aaagtattca gttcactaaa aagcaatgag 1080  
 atgctgttta gcatgtgccca agtcccccta gtgtgctggg ccgcgttgcac ttgtctgaag 1140  
 cagcaaatgg agaagggtgg tgatgtcaca ttgacctgcc aaacaaccac agctctgttt 1200  
 acctgcata tttctagctt gttcacacca gtagatggag gctctcctag tctacccaac 1260  
 caagcccagc tgagaagact gtgccaagtc gctgccaaag gaatatggac tatgacttac 1320  
 gtgtttaca gagaaaatct cagaaggctt gggtaactc aatctgtatgt ctctagttt 1380  
 atggacagca atattattca gaaggacgcgca gагтатгaaa actgctatgt gttcacccac 1440  
 ctcatgttc aggagtttt tgcatgtatg ttctatatgt tgaaaggcag ttggaaagct 1500  
 gggAACCCCTT CCTGCCAGCC TTTGAAGAT TTGAAGTCAT TACTTCAAAG CACAAGTTAT 1560  
 AAAGACCCCCC ATTGACACA GATGAAGTGC TTTTGTGG GCCTTTGAA TGAAGATCGA 1620  
 GTAAAACAAC TGGAGAGGAC TTTTAACTGT AAAATGTCAC TGAAGATAAA ATCAAAGTTA 1680  
 CTTCAGTGTA TGGAAAGTATT AGGAAACAGT GACTATTCTC CATCACAGCT GGGATTCTG 1740  
 GAGTTGTTCTC ACTGTCTGTA TGAGACTCAA GATAAAGCGT TTATAAGCCA GGCAATGAGA 1800  
 TGTTTCCCAA AGGTTGCCAT TAATATTGT GAGAAAATAC ATTGCTTGT ATCTTCTTC 1860  
 TGCCCTTAAGC ACTGCCGGTG TTTGCGGACC ATCAGGCTGT CTGTAACTGT GGTATTGAG 1920  
 AAGAAGATAT TAAAAACAAG CCTCCCAACT AACACTTGGT TGAAATTAT CACTTCCCT 1980  
 GATGGTTGTC AGGATATCTC TACTTCTTC ATTCTAAACA AGAATCTGAT GCATCTTGAC 2040  
 CTAAGGGAA GTGATATAGG GGATAATGGA GTAAAGTCAT TGTGTGAGGC CTTGAAACAC 2100  
 CCAGAGTGTA AACTACAGAC TCTCAGGCTG GAATCTGCA ACCTAACTGT ATTGTTGT 2160  
 CTAATATAT CTAATGCTCT CATCAGAAGC CAGAGCCTGA TATTCTGAA TCTGTCAACC 2220  
 AATAATCTGT TGGATGATGG AGTGCAGCTT TTGTGTGAGG CCTTAAGACA TCCAAAGTGT 2280  
 TATCTAGAGA GACTGTCCTT AGAAAGCTGT GGTCTCACAG AGGCTGGCTG TGAGTATCTT 2340  
 TCTTGGCTC TCATCAGCAA TAAAAGACTG ACACATTGT GCTTGGCAGA CAATGTCTG 2400  
 GGTGATGGTG GAGTAAAGCT TATGAGTGTAT GCCCTGCAAC ATGCACAAATG TACTCTGAA 2460  
 AGCCTTGTGC TGAGGCCTTG CCATTCACT TCACCTGCA GTGAATATCT GTCAACTTCT 2520  
 CTTCTACACA ACAAGAGCCT GACGCATCTG GATCTAGGAT CAAACTGGCT ACAAGACAA 2580  
 GGAGTGAAGC TTCTGTGTGA TGTCTTCGG CATCCAAGCT GTAATCTCA GGACTTGGAA 2640  
 TTGATGGGCT GTGTTCTCAC TAATGCTGT TGTCTGGATC TGGCTTGTATTTGAAT 2700

aacccaaacc tgaggagcct ggaccttggg aacaacgatt tgcaggatga tggagtgaaa 2760  
attctgtgtg atgccttgag atatccaaac tgtaacattc agaggctcg gttggaatac 2820  
tgtggttga catctctctg ctgtcaagat ctctcctctg ctcttatctg caacaaaaga 2880  
ctgataaaaaa tgaatctgac acagaatacc ttaggatatg aaggaattgt gaagttatat 2940  
aaagtottga agtctcctaa gtgtaaacta caagttctag gacaacagga tttccaagct 3000  
gcccaaggaa aactccaaca aagagctggc tctggatga 3039

<210> 12  
<211> 1012  
<212> PRT  
<213> Homo sapiens

<400> 12

Met Ala Asp Ser Ser Ser Ser Phe Phe Pro Asp Phe Gly Leu Leu  
1 5 10 15

Leu Tyr Leu Glu Glu Leu Asn Lys Glu Glu Leu Asn Thr Phe Lys Leu  
20 25 30

Phe Leu Lys Glu Thr Met Glu Pro Glu His Gly Leu Thr Pro Trp Asn  
35 40 45

Glu Val Lys Lys Ala Arg Arg Glu Asp Leu Ala Asn Leu Met Lys Lys  
50 55 60

Tyr Tyr Pro Gly Glu Lys Ala Trp Ser Val Ser Leu Lys Ile Phe Gly  
65 70 75 80

Lys Met Asn Leu Lys Asp Leu Cys Glu Arg Ala Lys Glu Glu Ile Asn  
85 90 95

Trp Ser Ala Gln Thr Ile Gly Pro Asp Asp Ala Lys Ala Gly Glu Thr  
100 105 110

Gln Glu Asp Gln Glu Ala Val Leu Gly Asp Gly Thr Glu Tyr Arg Asn  
115 120 125

Arg Ile Lys Glu Lys Phe Cys Ile Thr Trp Asp Lys Lys Ser Leu Ala  
130 135 140

Gly Lys Pro Glu Asp Phe His His Gly Ile Ala Glu Lys Asp Arg Lys  
145 150 155 160

Leu Leu Glu His Leu Phe Asp Val Asp Val Lys Thr Gly Ala Gln Pro  
165 170 175

Gln Ile Val Val Leu Gln Gly Ala Ala Gly Val Gly Lys Thr Thr Leu  
180 185 190

Val Arg Lys Ala Met Leu Asp Trp Ala Glu Gly Ser Leu Tyr Gln Gln  
195 200 205

Arg Phe Lys Tyr Val Phe Tyr Leu Asn Gly Arg Glu Ile Asn Gln Leu  
210 215 220

Lys Glu Arg Ser Phe Ala Gln Leu Ile Ser Lys Asp Trp Pro Ser Thr  
225 230 235 240

Glu Gly Pro Ile Glu Glu Ile Met Tyr Gln Pro Ser Ser Leu Leu Phe  
245 250 255

Ile Ile Asp Ser Phe Asp Glu Leu Asn Phe Ala Phe Glu Glu Pro Glu  
260 265 270

Phe Ala Leu Cys Glu Asp Trp Thr Gln Glu His Pro Val Ser Phe Leu  
275 280 285

Met Ser Ser Leu Leu Arg Lys Val Met Leu Pro Glu Ala Ser Leu Leu  
290 295 300

Val Thr Thr Arg Leu Thr Thr Ser Lys Arg Leu Lys Gln Leu Leu Lys  
305 310 315 320

Asn His His Tyr Val Glu Leu Leu Gly Met Ser Glu Asp Ala Arg Glu  
325 330 335

Glu Tyr Ile Tyr Gln Phe Phe Glu Asp Lys Arg Trp Ala Met Lys Val  
340 345 350

Phe Ser Ser Leu Lys Ser Asn Glu Met Leu Phe Ser Met Cys Gln Val  
355 360 365

Pro Leu Val Cys Trp Ala Ala Cys Thr Cys Leu Lys Gln Gln Met Glu  
370 375 380

Lys Gly Gly Asp Val Thr Leu Thr Cys Gln Thr Thr Ala Leu Phe  
385 390 395 400

Thr Cys Tyr Ile Ser Ser Leu Phe Thr Pro Val Asp Gly Gly Ser Pro

405

410

415

Ser Leu Pro Asn Gln Ala Gln Leu Arg Arg Leu Cys Gln Val Ala Ala  
420 425 430

Lys Gly Ile Trp Thr Met Thr Tyr Val Phe Tyr Arg Glu Asn Leu Arg  
435 440 445

Arg Leu Gly Leu Thr Gln Ser Asp Val Ser Ser Phe Met Asp Ser Asn  
450 455 460

Ile Ile Gln Lys Asp Ala Glu Tyr Glu Asn Cys Tyr Val Phe Thr His  
465 470 475 480

Leu His Val Gln Glu Phe Phe Ala Ala Met Phe Tyr Met Leu Lys Gly  
485 490 495

Ser Trp Glu Ala Gly Asn Pro Ser Cys Gln Pro Phe Glu Asp Leu Lys  
500 505 510

Ser Leu Leu Gln Ser Thr Ser Tyr Lys Asp Pro His Leu Thr Gln Met  
515 520 525

Lys Cys Phe Leu Phe Gly Leu Leu Asn Glu Asp Arg Val Lys Gln Leu  
530 535 540

Glu Arg Thr Phe Asn Cys Lys Met Ser Leu Lys Ile Lys Ser Lys Leu  
545 550 555 560

Leu Gln Cys Met Glu Val Leu Gly Asn Ser Asp Tyr Ser Pro Ser Gln  
565 570 575

Leu Gly Phe Leu Glu Leu Phe His Cys Leu Tyr Glu Thr Gln Asp Lys  
580 585 590

Ala Phe Ile Ser Gln Ala Met Arg Cys Phe Pro Lys Val Ala Ile Asn  
595 600 605

Ile Cys Glu Lys Ile His Leu Leu Val Ser Ser Phe Cys Leu Lys His  
610 615 620

Cys Arg Cys Leu Arg Thr Ile Arg Leu Ser Val Thr Val Val Phe Glu  
625 630 635 640

Lys Lys Ile Leu Lys Thr Ser Leu Pro Thr Asn Thr Trp Leu Lys Phe  
645 650 655

Ile Thr Phe Pro Asp Gly Cys Gln Asp Ile Ser Thr Ser Leu Ile His  
660 665 670

Asn Lys Asn Leu Met His Leu Asp Leu Lys Gly Ser Asp Ile Gly Asp  
675 680 685

Asn Gly Val Lys Ser Leu Cys Glu Ala Leu Lys His Pro Glu Cys Lys  
690 695 700

Leu Gln Thr Leu Arg Leu Glu Ser Cys Asn Leu Thr Val Phe Cys Cys  
705 710 715 720

Leu Asn Ile Ser Asn Ala Leu Ile Arg Ser Gln Ser Leu Ile Phe Leu  
725 730 735

Asn Leu Ser Thr Asn Asn Leu Leu Asp Asp Gly Val Gln Leu Leu Cys  
740 745 750

Glu Ala Leu Arg His Pro Lys Cys Tyr Leu Glu Arg Leu Ser Leu Glu  
755 760 765

Ser Cys Gly Leu Thr Glu Ala Gly Cys Glu Tyr Leu Ser Leu Ala Leu  
770 775 780

Ile Ser Asn Lys Arg Leu Thr His Leu Cys Leu Ala Asp Asn Val Leu  
785 790 795 800

Gly Asp Gly Gly Val Lys Leu Met Ser Asp Ala Leu Gln His Ala Gln  
805 810 815

Cys Thr Leu Lys Ser Leu Val Leu Arg Arg Cys His Phe Thr Ser Leu  
820 825 830

Ser Ser Glu Tyr Leu Ser Thr Ser Leu Leu His Asn Lys Ser Leu Thr  
835 840 845

His Leu Asp Leu Gly Ser Asn Trp Leu Gln Asp Asn Gly Val Lys Leu  
850 855 860

Leu Cys Asp Val Phe Arg His Pro Ser Cys Asn Leu Gln Asp Leu Glu  
865 870 875 880

Leu Met Gly Cys Val Leu Thr Asn Ala Cys Cys Leu Asp Leu Ala Ser  
885 890 895

Val Ile Leu Asn Asn Pro Asn Leu Arg Ser Leu Asp Leu Gly Asn Asn  
900 905 910

Asp Leu Gln Asp Asp Gly Val Lys Ile Leu Cys Asp Ala Leu Arg Tyr  
915 920 925

Pro Asn Cys Asn Ile Gln Arg Leu Gly Leu Glu Tyr Cys Gly Leu Thr  
930 935 940

Ser Leu Cys Cys Gln Asp Leu Ser Ser Ala Leu Ile Cys Asn Lys Arg  
945 950 955 960

Leu Ile Lys Met Asn Leu Thr Gln Asn Thr Leu Gly Tyr Glu Gly Ile  
965 970 975

Val Lys Leu Tyr Lys Val Leu Lys Ser Pro Lys Cys Lys Leu Gln Val  
980 985 990

Leu Gly Gln Gln Asp Phe Gln Ala Ala Gln Gly Lys Leu Gln Gln Arg  
995 1000 1005

Ala Gly Ser Gly  
1010

<210> 13  
<211> 2808  
<212> DNA  
<213> Homo sapiens

<400> 13	
atggcagatt catcatcatc ttctttcttt cctgattttg ggctgctatt gtatttggag	60
gagctaaaca aagaggaatt aaatacattc aagttattcc taaaaggagac catggAACCT	120
gagcatggcc tgacaccctg gaatgaagtg aagaaggcca ggcgggagga cctggccaat	180
ttgatgaaga aatatttatcc aggagagaaa gcctggagtg tgtctctcaa aatctttggc	240
aagatgaacc tgaaggatct gtgtgagaga gcgaaagaag agatcaactg gtcggcccag	300
actataggac cagatgatgc caaggctgga gagacacaag aagatcagga ggcagtgctg	360
ggtgatggaa cagaatacag aaatagaata aaggaaaaat tttgcatcac ttgggacaag	420
aagtctttgg ctggaaagcc tgaagatttc catcatggaa ttgcagagaa agatagaaaa	480
ctgttggAAC acttgttgcA tgtggatgtc aaaaccggtg cacagccaca gatcgtgg	540
cttcaggggag ctgctggagt tggaaaaca accttggta gaaaggcaat gtttagattgg	600
gcagagggca gtctctacca gcagaggTTT aagtatgttt tttatctcaa tgggagagaa	660

attaaccagc	tgaaagagag	aagcttgct	caattgatat	caaaggactg	gcccaacaca	720
aaagccccca	ttgaagaaat	catgtaccag	ccaagtagcc	tcttgttat	tatagacagt	780
ttcgatgaac	tgaactttgc	cttgaaagaa	cctgagttg	cactgtgcga	agactggacc	840
caagacaacc	cagtgtcctt	cctcatgagt	agtttgctga	ggaaaagtgat	gctccctgag	900
gcatccttat	tggtgacaac	aagactcaca	acttctaaga	gactaaagca	gttgttgaag	960
aatcaccatt	atgttagagct	actaggaatg	tctgaggatg	caagagagga	gtatatttac	1020
cagtttttg	aagataagag	gtgggccatg	aaagtattca	gttcactaaa	aagcaatgag	1080
atgctgttta	gcatgtgccca	agtcccccta	gtgtgctggg	ccgcttgtac	ttgtctgaag	1140
cagcaaatgg	agaagggtgg	tgatgtcaca	ttgacctgcc	aaacaaccac	agctctgttt	1200
acctgctata	tttctagctt	gttcacacca	gtagatggag	gctctcctag	tctacccaac	1260
caagcccagc	tgagaagact	gtgccaagtc	gctgccaaag	gaatatggac	tatgacttac	1320
gtgtttaca	gagaaaatct	cagaaggctt	gggttaactc	aatctgatgt	ctctagttt	1380
atggacagca	atattattca	gaaggacgca	gagttatgaaa	actgctatgt	gttcacccac	1440
cttcatgttc	aggagttttt	tgcagctatg	ttctatatgt	tgaagggcag	ttgggaagct	1500
gggaaccctt	cctgccagcc	tttgaagat	ttgaagtcat	tacttcaaag	cacaagttat	1560
aaagacccccc	atttgacaca	gatgaagtgc	ttttgtttg	gcctttgaa	tgaagatcga	1620
gtaaaacaac	tggagaggac	ttttaactgt	aaaatgtcac	tgaagataaa	atcaaagtta	1680
cttcagtgtt	tggaagtatt	aggaaacagt	gactattctc	catcacagct	gggatttctg	1740
gagttgttcc	actgtctgtt	tgagactcaa	gataaagcgt	ttataagcca	ggcaatgaga	1800
tgtttcccaa	agggtgccat	taatatttgc	gagaaaatac	attggcttgt	atcttcttcc	1860
tgccttaagc	actgccgatg	tttgcagacc	atcaggctgt	ctgtaactgt	gctatttgag	1920
aagaagacat	taaaaacaag	cctcccaact	aacacttggg	atggtgatcg	cattactcac	1980
tgttgaaag	atctctgttc	tgtgcttcat	acaaatgaac	acttgagaga	attggacctg	2040
taccatagca	accttgataa	atcagcaatg	aatatcctgc	atcatgaact	aagccaccca	2100
aactgtaaac	tacaaaaact	actgttggaa	tttatactt	tccctgatgg	ttgtcaggat	2160
atctctactt	cttgattca	taacaagaat	ctgatgcattc	ttgacctaaa	agggagtgat	2220
atagggata	atggagtaaa	gtcattgtgt	gaggccttga	aacacccaga	gtgtaaacta	2280
cagactctca	gcttagaaag	ctgtggtctc	acagaggctg	gctgtgagta	tcttttttg	2340
gctctcatca	gcaataaaag	actgacacat	ttgtgcttgg	cagacaatgt	cttgggtgat	2400
ggtggagtaa	agcttatgag	tgatgccctg	caacatgcac	aatgtactct	gaagagcctt	2460
gtgctgaggc	gttgcattt	cacttcactt	agcagtgaat	atctgtcaac	ttcttcttcta	2520

cacaacaaga gcctgacgca tctggatcta gatatcaaact ggctacaaga caatggagtg 2580  
aagcttctgt gtgatgtctt tcggcatcca agctgtaatc ttcaggactt ggaattgatg 2640  
ggctgtgttc tcactaatgc atgttgtctg gatctggctt ctgttatttt gaataaccca 2700  
aacctgagga gcctggacct tggaaacaac gatttgcagg atgatggagt gaaaattctg 2760  
tgtgatgctt tgagatatcc aaactgtaac attcagaggc tcgggtga 2808

<210> 14  
<211> 935  
<212> PRT  
<213> Homo sapiens  
  
<400> 14

Met Ala Asp Ser Ser Ser Ser Phe Phe Pro Asp Phe Gly Leu Leu  
1 5 10 15

Leu Tyr Leu Glu Glu Leu Asn Lys Glu Glu Leu Asn Thr Phe Lys Leu  
20 25 30

Phe Leu Lys Glu Thr Met Glu Pro Glu His Gly Leu Thr Pro Trp Asn  
35 40 45

Glu Val Lys Lys Ala Arg Arg Glu Asp Leu Ala Asn Leu Met Lys Lys  
50 55 60

Tyr Tyr Pro Gly Glu Lys Ala Trp Ser Val Ser Leu Lys Ile Phe Gly  
65 70 75 80

Lys Met Asn Leu Lys Asp Leu Cys Glu Arg Ala Lys Glu Glu Ile Asn  
85 90 95

Trp Ser Ala Gln Thr Ile Gly Pro Asp Asp Ala Lys Ala Gly Glu Thr  
100 105 110

Gln Glu Asp Gln Glu Ala Val Leu Gly Asp Gly Thr Glu Tyr Arg Asn  
115 120 125

Arg Ile Lys Glu Lys Phe Cys Ile Thr Trp Asp Lys Lys Ser Leu Ala  
130 135 140

Gly Lys Pro Glu Asp Phe His His Gly Ile Ala Glu Lys Asp Arg Lys  
145 150 155 160

Leu Leu Glu His Leu Phe Asp Val Asp Val Lys Thr Gly Ala Gln Pro  
165 170 175

Gln Ile Val Val Leu Gln Gly Ala Ala Gly Val Gly Lys Thr Thr Leu  
180 185 190

Val Arg Lys Ala Met Leu Asp Trp Ala Glu Gly Ser Leu Tyr Gln Gln  
195 200 205

Arg Phe Lys Tyr Val Phe Tyr Leu Asn Gly Arg Glu Ile Asn Gln Leu  
210 215 220

Lys Glu Arg Ser Phe Ala Gln Leu Ile Ser Lys Asp Trp Pro Asn Thr  
225 230 235 240

Lys Ala Pro Ile Glu Glu Ile Met Tyr Gln Pro Ser Ser Leu Leu Phe  
245 250 255

Ile Ile Asp Ser Phe Asp Glu Leu Asn Phe Ala Phe Glu Glu Pro Glu  
260 265 270

Phe Ala Leu Cys Glu Asp Trp Thr Gln Asp Asn Pro Val Ser Phe Leu  
275 280 285

Met Ser Ser Leu Leu Arg Lys Val Met Leu Pro Glu Ala Ser Leu Leu  
290 295 300

Val Thr Thr Arg Leu Thr Thr Ser Lys Arg Leu Lys Gln Leu Leu Lys  
305 310 315 320

Asn His His Tyr Val Glu Leu Leu Gly Met Ser Glu Asp Ala Arg Glu  
325 330 335

Glu Tyr Ile Tyr Gln Phe Phe Glu Asp Lys Arg Trp Ala Met Lys Val  
340 345 350

Phe Ser Ser Leu Lys Ser Asn Glu Met Leu Phe Ser Met Cys Gln Val  
355 360 365

Pro Leu Val Cys Trp Ala Ala Cys Thr Cys Leu Lys Gln Gln Met Glu  
370 375 380

Lys Gly Gly Asp Val Thr Leu Thr Cys Gln Thr Thr Thr Ala Leu Phe  
385 390 395 400

Thr Cys Tyr Ile Ser Ser Leu Phe Thr Pro Val Asp Gly Gly Ser Pro  
405 410 415

Ser Leu Pro Asn Gln Ala Gln Leu Arg Arg Leu Cys Gln Val Ala Ala  
420 425 430

Lys Gly Ile Trp Thr Met Thr Tyr Val Phe Tyr Arg Glu Asn Leu Arg  
435 440 445

Arg Leu Gly Leu Thr Gln Ser Asp Val Ser Ser Phe Met Asp Ser Asn  
450 455 460

Ile Ile Gln Lys Asp Ala Glu Tyr Glu Asn Cys Tyr Val Phe Thr His  
465 470 475 480

Leu His Val Gln Glu Phe Phe Ala Ala Met Phe Tyr Met Leu Lys Gly  
485 490 495

Ser Trp Glu Ala Gly Asn Pro Ser Cys Gln Pro Phe Glu Asp Leu Lys  
500 505 510

Ser Leu Leu Gln Ser Thr Ser Tyr Lys Asp Pro His Leu Thr Gln Met  
515 520 525

Lys Cys Phe Leu Phe Gly Leu Leu Asn Glu Asp Arg Val Lys Gln Leu  
530 535 540

Glu Arg Thr Phe Asn Cys Lys Met Ser Leu Lys Ile Lys Ser Lys Leu  
545 550 555 560

Leu Gln Cys Met Glu Val Leu Gly Asn Ser Asp Tyr Ser Pro Ser Gln  
565 570 575

Leu Gly Phe Leu Glu Leu Phe His Cys Leu Tyr Glu Thr Gln Asp Lys  
580 585 590

Ala Phe Ile Ser Gln Ala Met Arg Cys Phe Pro Lys Val Ala Ile Asn  
595 600 605

Ile Cys Glu Lys Ile His Trp Leu Val Ser Ser Phe Cys Leu Lys His  
610 615 620

Cys Arg Cys Leu Gln Thr Ile Arg Leu Ser Val Thr Val Leu Phe Glu  
625 630 635 640

Lys Lys Thr Leu Lys Thr Ser Leu Pro Thr Asn Thr Trp Asp Gly Asp  
645 650 655

Arg Ile Thr His Cys Trp Lys Asp Leu Cys Ser Val Leu His Thr Asn  
660 665 670

Glu His Leu Arg Glu Leu Asp Leu Tyr His Ser Asn Leu Asp Lys Ser  
675 680 685

Ala Met Asn Ile Leu His His Glu Leu Ser His Pro Asn Cys Lys Leu  
690 695 700

Gln Lys Leu Leu Leu Lys Phe Ile Thr Phe Pro Asp Gly Cys Gln Asp  
705 710 715 720

Ile Ser Thr Ser Leu Ile His Asn Lys Asn Leu Met His Leu Asp Leu  
725 730 735

Lys Gly Ser Asp Ile Gly Asp Asn Gly Val Lys Ser Leu Cys Glu Ala  
740 745 750

Leu Lys His Pro Glu Cys Lys Leu Gln Thr Leu Ser Leu Glu Ser Cys  
755 760 765

Gly Leu Thr Glu Ala Gly Cys Glu Tyr Leu Ser Leu Ala Leu Ile Ser  
770 775 780

Asn Lys Arg Leu Thr His Leu Cys Leu Ala Asp Asn Val Leu Gly Asp  
785 790 795 800

Gly Gly Val Lys Leu Met Ser Asp Ala Leu Gln His Ala Gln Cys Thr  
805 810 815

Leu Lys Ser Leu Val Leu Arg Arg Cys His Phe Thr Ser Leu Ser Ser  
820 825 830

Glu Tyr Leu Ser Thr Ser Leu Leu His Asn Lys Ser Leu Thr His Leu  
835 840 845

Asp Leu Gly Ser Asn Trp Leu Gln Asp Asn Gly Val Lys Leu Leu Cys  
850 855 860

Asp Val Phe Arg His Pro Ser Cys Asn Leu Gln Asp Leu Glu Leu Met  
865 870 875 880

Gly Cys Val Leu Thr Asn Ala Cys Cys Leu Asp Leu Ala Ser Val Ile  
885 890 895

Leu Asn Asn Pro Asn Leu Arg Ser Leu Asp Leu Gly Asn Asn Asp Leu

900

905

910

Gln Asp Asp Gly Val Lys Ile Leu Cys Asp Ala Leu Arg Tyr Pro Asn  
915 920 925

Cys Asn Ile Gln Arg Leu Gly  
930 935

<210> 15  
<211> 2612  
<212> DNA  
<213> *Homo sapiens*

<400> 15  
aagctataca gcggcaccgc cggaacctgg ctgagtggtt cagccggctg cccagggagg 60  
acgcgcaggta tggcccaacc ttgcgcctag acacggtcca cggtgaccct gtatccgcg 120  
agagtacccc ttagtgagcta cttcgccac ccgcggagct ggccttggag catcagccac 180  
cccaggccgg gctccccca ctggccttgt ctcagcttt taacccggat gcctgtggc 240  
gccgggtgca gacagtggtg ctgtatggta cagtggcac aggcaagagc acgctggtgc 300  
gcaagatggt tctggactgg tgttatggc ggctgcccgc cttcgagctg ctcatcccc 360  
tctcctgtga ggacctgtca tccctggcc ctgccccagc ctccctgtgc caacttgtgg 420  
cccagcgcta cacgccccctg aaggagggttc tgccctgtat ggctgctgct gggtcccacc 480  
tcctcttgc gctccatggc ttagagcatc tcaacctcga cttccggctg gcaggcacgg 540  
gactttgttag tgacccggag gaaccgcagg aaccagctgc tatcategtc aacctgctgc 600  
gcaaatacat gctgcctcag gccagcattc tggtgaccac tcggccctct gccattggcc 660  
gtatccccag caagtacgtg ggccgctatg gtgagatctg cgggttctct gataccaacc 720  
tgcagaagct ctacttccag ctccgcctca accagccgtt ctgcgggtat gccgttggcg 780  
gttcagggtgt ctctgccaca ccagctcagc gtgaccacct ggtgcagatg ctctccgg 840  
acctggaggg gcaccaccag atagccgctg cctgcttctt gccgtcctat tgctggctcg 900  
tttgtgccac ctgcacttc ctgcattttt ccacgcctgc tggcagacc cttacaagca 960  
tctataccag ctccctgcgc ctcaacttca gcggggaaac cctggacagc actgaccct 1020  
ccaatttgc cctgatggcc tatgcagccc gaaccatggg caagttggcc tatgaggggg 1080  
tgtcctcccg caagacctac ttctctgaag aggtatgtctg tggctgcctg gaggctggca 1140  
tcaggacgga ggaggagttt cagctgctgc acatcttccg tcgggatgcc ctgaggtttt 1200  
tcctggccccc atgtgtggag ccagggcgtt cagggcacctt cgtgttcacc gtgcccggca 1260  
tgcaggaata cctggctgcc ctctacattt tgctgggttt gcgcaagacg accctgcaaa 1320

aggtgggcaa ggaagtggct gagctcgtagg gccgtgttgg ggaggacgtc agcctggtag 1380  
 tgggcattcat ggccaagctg ctgcctctgc gggctctgcc tctgctcttc aacctgatca 1440  
 aggtggttcc acgagtggtt gggcgcatgg tggtaaaag ccgggaggcg gtggctcagg 1500  
 ccatggtgct ggagatgttt cgagaggagg actactaca cgatgatgtt ctggaccaga 1560  
 tgggcgccag tatcctgggc gtggagggcc cccggcgcca cccagatgag ccccctgagg 1620  
 atgaagtctt cgagctcttc cccatgttca tggggggct tctctctgcc cacaaccgag 1680  
 ctgtgctagc tcagcttggc tgccccatca agaacctgga tgccctggag aatgcccagg 1740  
 ccatcaagaa gaagctggc aagctggcc ggcaggtgct gccccatca gagctocttg 1800  
 accacotctt cttccactat gagttccaga accagcgctt ctccgctgag gtgctcagct 1860  
 ccctgcgtca gctcaacctg gcaggtgtgc gcatgacacc agtcaagtgc acagtggtag 1920  
 cagctgtgct gggcagcgga aggcatgccc tggatgaggt gaacttggcc tcctgccagc 1980  
 tagatcctgc tggctgcgc acactcctgc ctgtcttct gcgtgcccgg aagctggct 2040  
 tgcaactcaa cagcctggc cctgaggcct gcaaggacct ccgagacctg ttgctgcatg 2100  
 accagtgcca aattaccaca ctgcggctgt ccaacaaccc gctgacggcg gcaggcctgg 2160  
 agctgctggc tgcccagctg gaccgcaacc ggcagctgca ggagctgaac gtggcgtaca 2220  
 acggtgctgg tgacacagcg gcccggccc tggccagagc tgcccgaggag cacccttccc 2280  
 tggactgct acaagctcta ctgaatggca tcgactttct ctctcctgcc agcctctact 2340  
 tcaatgagct gagctcagag gcccggcagg tcttgcgaga cttgggggggt gctgctgaag 2400  
 gtggtgcccgg ggtgggtggtg tcactgacag aggggacggc ggtgtcagaa tactggtcag 2460  
 tgatcctcag tgaagtccag cggAACCTCA atagctggaa tcggggcccgg gttcagcgac 2520  
 accttgagct cctactgcgg gatctggaag atagccgggg tgccaccctt aatccttggc 2580  
 gcaaggccca gctgctgcga gtggaggcg ag 2612

<210> 16  
 <211> 870  
 <212> PRT  
 <213> Homo sapiens

<400> 16

Ala	Ile	Gln	Arg	His	Arg	Arg	Asn	Leu	Ala	Glu	Trp	Phe	Ser	Arg	Leu
1								10						15	

Pro	Arg	Glu	Glu	Arg	Gln	Phe	Gly	Pro	Thr	Phe	Ala	Leu	Asp	Thr	Val
								20					25		30

His Val Asp Pro Val Ile Arg Glu Ser Thr Pro Asp Glu Leu Leu Arg

35

40

45

Pro Pro Ala Glu Leu Ala Leu Glu His Gln Pro Pro Gln Ala Gly Leu  
50 55 60

Pro Pro Leu Ala Leu Ser Gln Leu Phe Asn Pro Asp Ala Cys Gly Arg  
65 70 75 80

Arg Val Gln Thr Val Val Leu Tyr Gly Thr Val Gly Thr Gly Lys Ser  
85 90 95

Thr Leu Val Arg Lys Met Val Leu Asp Trp Cys Tyr Gly Arg Leu Pro  
100 105 110

Ala Phe Glu Leu Leu Ile Pro Phe Ser Cys Glu Asp Leu Ser Ser Leu  
115 120 125

Gly Pro Ala Pro Ala Ser Leu Cys Gln Leu Val Ala Gln Arg Tyr Thr  
130 135 140

Pro Leu Lys Glu Val Leu Pro Leu Met Ala Ala Ala Gly Ser His Leu  
145 150 155 160

Leu Phe Val Leu His Gly Leu Glu His Leu Asn Leu Asp Phe Arg Leu  
165 170 175

Ala Gly Thr Gly Leu Cys Ser Asp Pro Glu Glu Pro Gln Glu Pro Ala  
180 185 190

Ala Ile Ile Val Asn Leu Leu Arg Lys Tyr Met Leu Pro Gln Ala Ser  
195 200 205

Ile Leu Val Thr Thr Arg Pro Ser Ala Ile Gly Arg Ile Pro Ser Lys  
210 215 220

Tyr Val Gly Arg Tyr Gly Glu Ile Cys Gly Phe Ser Asp Thr Asn Leu  
225 230 235 240

Gln Lys Leu Tyr Phe Gln Leu Arg Leu Asn Gln Pro Tyr Cys Gly Tyr  
245 250 255

Ala Val Gly Gly Ser Gly Val Ser Ala Thr Pro Ala Gln Arg Asp His  
260 265 270

Leu Val Gln Met Leu Ser Arg Asn Leu Glu Gly His His Gln Ile Ala  
275 280 285

Ala Ala Cys Phe Leu Pro Ser Tyr Cys Trp Leu Val Cys Ala Thr Leu  
290 295 300

His Phe Leu His Ala Pro Thr Pro Ala Gly Gln Thr Leu Thr Ser Ile  
305 310 315 320

Tyr Thr Ser Phe Leu Arg Leu Asn Phe Ser Gly Glu Thr Leu Asp Ser  
325 330 335

Thr Asp Pro Ser Asn Leu Ser Leu Met Ala Tyr Ala Ala Arg Thr Met  
340 345 350

Gly Lys Leu Ala Tyr Glu Gly Val Ser Ser Arg Lys Thr Tyr Phe Ser  
355 360 365

Glu Glu Asp Val Cys Gly Cys Leu Glu Ala Gly Ile Arg Thr Glu Glu  
370 375 380

Glu Phe Gln Leu Leu His Ile Phe Arg Arg Asp Ala Leu Arg Phe Phe  
385 390 395 400

Leu Ala Pro Cys Val Glu Pro Gly Arg Ala Gly Thr Phe Val Phe Thr  
405 410 415

Val Pro Ala Met Gln Glu Tyr Leu Ala Ala Leu Tyr Ile Val Leu Gly  
420 425 430

Leu Arg Lys Thr Thr Leu Gln Lys Val Gly Lys Glu Val Ala Glu Leu  
435 440 445

Val Gly Arg Val Gly Glu Asp Val Ser Leu Val Leu Gly Ile Met Ala  
450 455 460

Lys Leu Leu Pro Leu Arg Ala Leu Pro Leu Leu Phe Asn Leu Ile Lys  
465 470 475 480

Val Val Pro Arg Val Phe Gly Arg Met Val Gly Lys Ser Arg Glu Ala  
485 490 495

Val Ala Gln Ala Met Val Leu Glu Met Phe Arg Glu Glu Asp Tyr Tyr  
500 505 510

Asn Asp Asp Val Leu Asp Gln Met Gly Ala Ser Ile Leu Gly Val Glu  
515 520 525

Gly Pro Arg Arg His Pro Asp Glu Pro Pro Glu Asp Glu Val Phe Glu  
530 535 540

Leu Phe Pro Met Phe Met Gly Gly Leu Leu Ser Ala His Asn Arg Ala  
545 550 555 560

Val Leu Ala Gln Leu Gly Cys Pro Ile Lys Asn Leu Asp Ala Leu Glu  
565 570 575

Asn Ala Gln Ala Ile Lys Lys Leu Gly Lys Leu Gly Arg Gln Val  
580 585 590

Leu Pro Pro Ser Glu Leu Leu Asp His Leu Phe Phe His Tyr Glu, Phe  
595 600 605

Gln Asn Gln Arg Phe Ser Ala Glu Val Leu Ser Ser Leu Arg Gln Leu  
610 615 620

Asn Leu Ala Gly Val Arg Met Thr Pro Val Lys Cys Thr Val Val Ala  
625 630 635 640

Ala Val Leu Gly Ser Gly Arg His Ala Leu Asp Glu Val Asn Leu Ala  
645 650 655

Ser Cys Gln Leu Asp Pro Ala Gly Leu Arg Thr Leu Leu Pro Val Phe  
660 665 670

Leu Arg Ala Arg Lys Leu Gly Leu Gln Leu Asn Ser Leu Gly Pro Glu  
675 680 685

Ala Cys Lys Asp Leu Arg Asp Leu Leu Leu His Asp Gln Cys Gln Ile  
690 695 700

Thr Thr Leu Arg Leu Ser Asn Asn Pro Leu Thr Ala Ala Gly Leu Glu  
705 710 715 720

Leu Leu Ala Ala Gln Leu Asp Arg Asn Arg Gln Leu Gln Glu Leu Asn  
725 730 735

Val Ala Tyr Asn Gly Ala Gly Asp Thr Ala Ala Leu Ala Leu Ala Arg  
740 745 750

Ala Ala Arg Glu His Pro Ser Leu Glu Leu Leu Gln Ala Leu Leu Asn  
755 760 765

Gly Ile Asp Phe Leu Ser Pro Ala Ser Leu Tyr Phe Asn Glu Leu Ser  
770 775 780

Ser Glu Gly Arg Gln Val Leu Arg Asp Leu Gly Gly Ala Ala Glu Gly  
785 790 795 800

Gly Ala Arg Val Val Val Ser Leu Thr Glu Gly Thr Ala Val Ser Glu  
805 810 815

Tyr Trp Ser Val Ile Leu Ser Glu Val Gln Arg Asn Leu Asn Ser Trp  
820 825 830

Asp Arg Ala Arg Val Gln Arg His Leu Glu Leu Leu Leu Arg Asp Leu  
835 840 845

Glu Asp Ser Arg Gly Ala Thr Leu Asn Pro Trp Arg Lys Ala Gln Leu  
850 855 860

Leu Arg Val Glu Gly Glu  
865 870

<210> 17  
<211> 3017  
<212> DNA  
<213> Homo sapiens

<400> 17  
atgaggtggg gcccaccattt gcccaggggcc tcttggggct ctggtttttag aagagcactc 60  
cagcgaccag atgatcgtat ccccttcctg atccactgga gttggccctt tcaaggggag 120  
cgtccctttg ggccccctag ggccttata cgccaccacg gaagctcggt agatagcgct 180  
cccccatccg ggaggcatgg acggctgttc cccagcgctt ctgcaactga agctatacag 240  
cggcacccgcc ggaacctggc tgagtggttc agccggctgc ccagggagga ggcgcagtt 300  
ggcccaacct ttgccttaga cacggtccac gttgaccctg tgatccgcga gagtaccct 360  
gatgagctac ttgccccacc cgcgagctg gccctggagc atcagccacc ccaggccggg 420  
ctccccccac tggccttgtc tcagctttt aacccggatg cctgtggcg ccgggtgcag 480  
acagtggtgc tgtatgggac agtgggcaca ggcaagagca cgctggtgcg caagatggtt 540  
ctggactggc gttatgggac gctggccggcc ttcgagctgc tcatccccctt ctccctgtgag 600  
gacctgtcat ccctggggcc tgccccagcc tccctgtgcc aacttgtggc ccagcgctac 660  
acgccccctga aggaggttct gcccctgatg gctgctgctg ggtccccacct cctctttgtg 720  
ctccatggct tagagcatct caaccccgac ttccggctgg cagggcacggg actttgttagt 780  
gaccggagg aaccgcagga accagctgct atcatcgta acctgctgctgca caaatacatg 840

ctgcctcagg ccagcattct ggtgaccact cggccctctg ccattggccg tatcccagc	900
aagtacgtgg gccgctatgg tgagatctgc ggtttctctg ataccaacct gcagaagctc	960
tacttcacgc tccgcctcaa ccagccgtac tgcggtatg ccgttggcgg ttcaggtgtc	1020
tctgccacac cagctcagcg tgaccacctg gtgcagatgc tctccggaa cctggagggg	1080
caccaccaga tagccgctgc ctgcttcctg ccgtcttatt gctggctcgt ttgtgccacc	1140
ttgcacttcc tgcatgcccc cacgcctgct gggcagaccc ttacaagcat ctataccagc	1200
ttcctgcgcc tcaacttcag cggggaaacc ctggacagca ctgaccctc caatttgtcc	1260
ctgatggcct atgcagcccc aaccatgggc aagttggcct atgagggggt gtcctccgc	1320
aagacctaact tctctgaaga ggatgtctgt ggctgcctgg aggctggcat caggacggag	1380
gaggagttc agctgctgca catctccgt cgggatgccc tgaggtttt cctggcccca	1440
tgtgtggagc cagggcgtgc aggcaccttc gtgttcaccg tgcccgccat gcaggaatac	1500
ctggctgccc tctacattgt gctgggtttgc caaagacga ccctgcaaaa ggtgggcaag	1560
gaagtggctg agctcgtgg ccgtgttggg gaggacgtca gcctggtaact gggcatcatg	1620
gccaagctgc tgcctctgca ggctctgcct ctgctcttca acctgatcaa ggtggttcca	1680
cgagtgttttgc ggcatgggtt gggtaaaagc cgggaggcgg tgactcaggc catggtgctg	1740
gagatgtttc gagaggagga ctactacaac gatgatgttc tggaccagat gggcgccagt	1800
atcctgggcg tggagggccc cggcgccac ccagatgagc cccctgagga tgaagtcttc	1860
gagctottcc ccatgttcat ggggggctt ctctctgccc acaaccgagc tgtgcttagct	1920
cagcttggct gccccatcaa gaacctggat gccctggaga atgcccaggc catcaagaag	1980
aagctggca agctggccg gcaggtgctg ccccatcag agctccttga ccacctttc	2040
ttccactatg agttccagaa ccagcgcttc tccgctgagg tgctcagctc cctgcgtcag	2100
ctcaacctgg caggtgtgca catgacacca gtcaagtgca cagtggtggc agctgtgctg	2160
ggcagcggaa ggcattgcctt ggtggatgg aacttggcct cctgcccagct agatcctgct	2220
gggctgcgc aactcctgca tgcgttgc cgtgcccggaa agctgggctt gcaactcaac	2280
agcctgggc ctgaggcctg caaggacctc cgagacctgt tgctgcatga ccagtgc当地	2340
attaccacac tgcggctgtc caacaacccg ctgacggagg caggtgttgc cgtgctaatg	2400
gaggggctgg caggaaacac ctcagtgacg cacctgtccc tgctgcacac gggccttggg	2460
gacgaaggcc tggagctgct ggctgcccag ctggaccgca accggcagct gcaggagctg	2520
aacgtggcgt acaacgggtgc tgggtacaca gcccggctgg ccctggccag agctgcccgg	2580
gagcaccctt ccctggaaact gctacacccctc tacttcaatg agctgagctc agagggccgc	2640

caggtcttgc gagacttggg gggtgctgct gaaggtggtg cccgggtggt ggtgtcaactg 2700  
acagagggga cggcggtgtc agaatactgg tcagtatcc tcagtgaagt ccagcggAAC 2760  
ctcaatacgct gggatcgggc cgggttcag cgacaccttg agctcctact gcgggatctg 2820  
gaagatagcc ggggtgccac ccttaatcct tgacgcaagg cccagctgct gcgagtgag 2880  
ggcgaggtca gggccctcct ggagcagctg ggaagctctg gaagctgaga cactggcggc 2940  
aggcacctag ctatgtgacc actggcccta aacctttcc ctctgtggcc tcctggcttg 3000  
cactgctccc tctagaa 3017

<210> 18  
<211> 950  
<212> PRT  
<213> Homo sapiens

<400> 18

Met Arg Trp Gly His His Leu Pro Arg Ala Ser Trp Gly Ser Gly Phe  
1 5 10 15

Arg Arg Ala Leu Gln Arg Pro Asp Asp Arg Ile Pro Phe Leu Ile His  
20 25 30

Trp Ser Trp Pro Leu Gln Gly Glu Arg Pro Phe Gly Pro Pro Arg Ala  
35 40 45

Phe Ile Arg His His Gly Ser Ser Val Asp Ser Ala Pro Pro Ser Gly  
50 55 60

Arg His Gly Arg Leu Phe Pro Ser Ala Ser Ala Thr Glu Ala Ile Gln  
65 70 75 80

Arg His Arg Arg Asn Leu Ala Glu Trp Phe Ser Arg Leu Pro Arg Glu  
85 90 95

Glu Arg Gln Phe Gly Pro Thr Phe Ala Leu Asp Thr Val His Val Asp  
100 105 110

Pro Val Ile Arg Glu Ser Thr Pro Asp Glu Leu Leu Arg Pro Pro Ala  
115 120 125

Glu Leu Ala Leu Glu His Gln Pro Pro Gln Ala Gly Leu Pro Pro Leu  
130 135 140

Ala Leu Ser Gln Leu Phe Asn Pro Asp Ala Cys Gly Arg Arg Val Gln  
145 150 155 160

Thr Val Val Leu Tyr Gly Thr Val Gly Thr Gly Lys Ser Thr Leu Val  
165 170 175

Arg Lys Met Val Leu Asp Trp Cys Tyr Gly Arg Leu Pro Ala Phe Glu  
180 185 190

Leu Leu Ile Pro Phe Ser Cys Glu Asp Leu Ser Ser Leu Gly Pro Ala  
195 200 205

Pro Ala Ser Leu Cys Gln Leu Val Ala Gln Arg Tyr Thr Pro Leu Lys  
210 215 220

Glu Val Leu Pro Leu Met Ala Ala Ala Gly Ser His Leu Leu Phe Val  
225 230 235 240

Leu His Gly Leu Glu His Leu Asn Leu Asp Phe Arg Leu Ala Gly Thr  
245 250 255

Gly Leu Cys Ser Asp Pro Glu Glu Pro Gln Glu Pro Ala Ala Ile Ile  
260 265 270

Val Asn Leu Leu Arg Lys Tyr Met Leu Pro Gln Ala Ser Ile Leu Val  
275 280 285

Thr Thr Arg Pro Ser Ala Ile Gly Arg Ile Pro Ser Lys Tyr Val Gly  
290 295 300

Arg Tyr Gly Glu Ile Cys Gly Phe Ser Asp Thr Asn Leu Gln Lys Leu  
305 310 315 320

Tyr Phe Gln Leu Arg Leu Asn Gln Pro Tyr Cys Gly Tyr Ala Val Gly  
325 330 335

Gly Ser Gly Val Ser Ala Thr Pro Ala Gln Arg Asp His Leu Val Gln  
340 345 350

Met Leu Ser Arg Asn Leu Glu Gly His His Gln Ile Ala Ala Ala Cys  
355 360 365

Phe Leu Pro Ser Tyr Cys Trp Leu Val Cys Ala Thr Leu His Phe Leu  
370 375 380

His Ala Pro Thr Pro Ala Gly Gln Thr Leu Thr Ser Ile Tyr Thr Ser  
385 390 395 400

Phe Leu Arg Leu Asn Phe Ser Gly Glu Thr Leu Asp Ser Thr Asp Pro  
405 410 415

Ser Asn Leu Ser Leu Met Ala Tyr Ala Ala Arg Thr Met Gly Lys Leu  
420 425 430

Ala Tyr Glu Gly Val Ser Ser Arg Lys Thr Tyr Phe Ser Glu Glu Asp  
435 440 445

Val Cys Gly Cys Leu Glu Ala Gly Ile Arg Thr Glu Glu Glu Phe Gln  
450 455 460

Leu Leu His Ile Phe Arg Arg Asp Ala Leu Arg Phe Phe Leu Ala Pro  
465 470 475 480

Cys Val Glu Pro Gly Arg Ala Gly Thr Phe Val Phe Thr Val Pro Ala  
485 490 495

Met Gln Glu Tyr Leu Ala Ala Leu Tyr Ile Val Leu Gly Leu Arg Lys  
500 505 510

Thr Thr Leu Gln Lys Val Gly Lys Glu Val Ala Glu Leu Val Gly Arg.  
515 520 525

Val Gly Glu Asp Val Ser Leu Val Leu Gly Ile Met Ala Lys Leu Leu  
530 535 540

Pro Leu Arg Ala Leu Pro Leu Leu Phe Asn Leu Ile Lys Val Val Pro  
545 550 555 560

Arg Val Phe Gly Arg Met Val Gly Lys Ser Arg Glu Ala Val Thr Gln  
565 570 575

Ala Met Val Leu Glu Met Phe Arg Glu Glu Asp Tyr Tyr Asn Asp Asp  
580 585 590

Val Leu Asp Gln Met Gly Ala Ser Ile Leu Gly Val Glu Gly Pro Arg  
595 600 605

Arg His Pro Asp Glu Pro Pro Glu Asp Glu Val Phe Glu Leu Phe Pro  
610 615 620

Met Phe Met Gly Gly Leu Leu Ser Ala His Asn Arg Ala Val Leu Ala  
625 630 635 640

Gln Leu Gly Cys Pro Ile Lys Asn Leu Asp Ala Leu Glu Asn Ala Gln

645

650

655

Ala Ile Lys Lys Lys Leu Gly Lys Leu Gly Arg Gln Val Leu Pro Pro  
660 665 670

Ser Glu Leu Leu Asp His Leu Phe Phe His Tyr Glu Phe Gln Asn Gln  
675 680 685

Arg Phe Ser Ala Glu Val Leu Ser Ser Leu Arg Gln Leu Asn Leu Ala  
690 695 700

Gly Val Arg Met Thr Pro Val Lys Cys Thr Val Val Ala Ala Val Leu  
705 710 715 720

Gly Ser Gly Arg His Ala Leu Asp Glu Val Asn Leu Ala Ser Cys Gln  
725 730 735

Leu Asp Pro Ala Gly Leu Arg Thr Leu Leu Pro Val Phe Leu Arg Ala  
740 745 750

Arg Lys Leu Gly Leu Gln Leu Asn Ser Leu Gly Pro Glu Ala Cys Lys  
755 760 765

Asp Leu Arg Asp Leu Leu Leu His Asp Gln Cys Gln Ile Thr Thr Leu  
770 775 780

Arg Leu Ser Asn Asn Pro Leu Thr Glu Ala Gly Val Ala Val Leu Met  
785 790 795 800

Glu Gly Leu Ala Gly Asn Thr Ser Val Thr His Leu Ser Leu Leu His  
805 810 815

Thr Gly Leu Gly Asp Glu Gly Leu Glu Leu Leu Ala Ala Gln Leu Asp  
820 825 830

Arg Asn Arg Gln Leu Gln Glu Leu Asn Val Ala Tyr Asn Gly Ala Gly  
835 840 845

Asp Thr Ala Ala Leu Ala Leu Ala Arg Ala Ala Arg Glu His Pro Ser  
850 855 860

Leu Glu Leu Leu His Leu Tyr Phe Asn Glu Leu Ser Ser Glu Gly Arg  
865 870 875 880

Gln Val Leu Arg Asp Leu Gly Gly Ala Ala Glu Gly Gly Ala Arg Val  
885 890 895

Val Val Ser Leu Thr Glu Gly Thr Ala Val Ser Glu Tyr Trp Ser Val  
900 905 910

Ile Leu Ser Glu Val Gln Arg Asn Leu Asn Ser Trp Asp Arg Ala Arg  
915 920 925

Val Gln Arg His Leu Glu Leu Leu Leu Arg Asp Leu Glu Asp Ser Arg  
930 935 940

Gly Ala Thr Leu Asn Pro  
945 950

<210> 19  
<211> 2800  
<212> DNA  
<213> Homo sapiens

<400> 19  
atgagatggg gccaccattt gcccagggcc tcttgggct ctggtttag aagagcactc 60  
cagcgaccag atgatcgat ccccttcctg atccactgga gttggccct tcaaggggag 120  
cgtcccttg ggccccctag ggccttata cgccaccacg gaagctcggt agatagcgct 180  
cccccatccg ggaggcatgg acggctgttc cccagcgct ctgcaactga agctatacag 240  
cggcaccgccc ggaacctggc tgagtggttc agccggctgc ccagggagga gcgccagtt 300  
ggcccaacct ttgccctaga cacggtccac gttgaccctg tgcactcgaa gagtaccct 360  
gatgagctac ttgccccacc cgcgagctg gcccggagc atcagccacc ccaggccggg 420  
ctccccccac tggccttgtc tcagctctt aacccggatg cctgtggcg ccgggtgcag 480  
acagtggtgc tgtatggcac agtgggcaca ggcaagagca cgctggtgcg caagatggtt 540  
ctggactggc gttatggcg gctgccggcc ttgcagctgc tcatccccctt ctccctgtgag 600  
gacctgtcat ccctggggcc tgccccagcc tccctgtgcc aacttgtggc ccagcgctac 660  
acgccccctga aggaggttct gcccctgatg gctgctgctg ggtcccaccc cctctttgtg 720  
ctccatggct tagagcatct caacctcgac ttccggctgg cagggcacggg actttgttagt 780  
gaccggagg aaccgcagga accagctgct atcatcgta acctgctgcg caaatacatg 840  
ctgcctcagg ccagcattct ggtgaccact cggccctctg ccattggccg tatccccagc 900  
aagtacgtgg gcccgtatgg tgagatctgc ggtttctctg ataccaacct gcagaagctc 960  
tacttccagg tccgcctcaa ccagccgtac tgcgggtatg ccgttggccg ttcaggtgtc 1020  
tctgccacac cagctcagcg tgaccacctg gtgcagatgc tctccggaa cctggagggg 1080  
caccaccaga tagccgctgc ctgccttcctg ccgtccattt gctggctcg tttgtgccacc 1140

ttgcacttcc	tgc	atgcccc	cacgcctgct	gggcagaccc	ttacaaggcat	ctataccagc	1200		
ttcctgcgcc	tca	acttcag	cgggaaacc	ctggacagca	ctgaccctc	caatttgcc	1260		
ctgatggcct	atgc	agccc	aaccatggc	aagttggct	atgaggggt	gtcctccgc	1320		
aagaccta	tct	ctgaaga	ggatgtctgt	ggctgcctgg	aggctggcat	caggacggag	1380		
gaggagttc	agct	gctgca	catcttccgt	cggatgccc	tgaggtttt	cctggccca	1440		
tgtgtggagc	cagg	gcgtgc	aggcacctc	gtgttacccg	tgccgc	ccat gcaggaatac	1500		
ctggctgccc	tct	acattgt	gctgggttt	cgcaagacga	ccctgcaaaa	ggtgggcaag	1560		
gaagtggctg	agct	cgtggg	ccgtgttggg	gaggacgtca	gcctggta	ct gggcatcatg	1620		
gccaagctgc	tgc	cctctgcg	ggctctgcct	ctgctcttca	acctgatcaa	ggtggttcca	1680		
cgagtgtttg	ggc	gcatgg	gggtaaaagc	cgggaggcgg	tgactcaggc	catggtgc	1740		
gagatgtttc	gag	aggagga	ctactacaac	gatgatttc	tggaccagat	gggcgc	1800		
atcctggcg	tgg	agggccc	ccggcgccac	ccagatgagc	cccctgagga	tgaagtcttc	1860		
gagctcttcc	ccat	gttcat	ggggggctt	ctctctgccc	acaaccgago	tgtgctagct	1920		
cagcttggct	gccc	catcaa	gaacctggat	gccctggaga	atgcccaggc	catcaagaag	1980		
aagctggca	agct	gggccc	gcagggtctg	ccccatcag	agctccttga	ccac	cttcc 2040		
ttccactatg	at	ttccagaa	ccagcgcttc	tccgctgagg	tgctcagctc	cctgcgtc	2100		
ctcaacctgg	cagg	gtgc	catgacacca	gtcaagtgc	cagtgg	ggc agctgtc	2160		
ggcagcggaa	ggc	atgc	ccct	ggatgaggtg	aacttggct	cctgccagct	agatcctgct	2220	
gggctgcgc	cact	cctg	tgt	ttccctg	cgtgccc	gaa	ctcaac	2280	
agcctggcc	ctg	aggc	ctc	caaggac	ctc	cgagac	ctgt	2340	
attaccacac	tg	cggt	gtgc	caacaaccc	ctgacggagg	cagg	gttgc	2400	
gaggggctgg	cagg	aaacac	ctc	agtgcac	cac	ctgt	gcacac	2460	
gacgaaggcc	tgg	agctg	ctc	gatgcac	ctgg	accgg	ccag	2520	
aacgtggcgt	aca	acgg	gtc	ttgcac	acc	ggcc	cttgg	2580	
gagcaccctt	ccct	ggaa	act	gtacagg	gtc	ggccat	cc	agatgtt	2640
ctcctgcctt	at	gctc	acac	gtgg	acacc	aggatgc	ccct	tttgc	2700
atcctcatgc	cc	cctt	ggcc	acaatgg	ttgg	cttgc	ccat	ttgg	2760
acctgacttgc	ctg	cttattaa	aaagccgtgt	gccttctacc					2800

<210> 20  
 <211> 932  
 <212> PRT

<213> Homo sapiens

<400> 20

Met Arg Trp Gly His His Leu Pro Arg Ala Ser Trp Gly Ser Gly Phe  
1 5 10 15

Arg Arg Ala Leu Gln Arg Pro Asp Asp Arg Ile Pro Phe Leu Ile His  
20 25 30

Trp Ser Trp Pro Leu Gln Gly Glu Arg Pro Phe Gly Pro Pro Arg Ala  
35 40 45

Phe Ile Arg His His Gly Ser Ser Val Asp Ser Ala Pro Pro Ser Gly  
50 55 60

Arg His Gly Arg Leu Phe Pro Ser Ala Ser Ala Thr Glu Ala Ile Gln  
65 70 75 80

Arg His Arg Arg Asn Leu Ala Glu Trp Phe Ser Arg Leu Pro Arg Glu  
85 90 95

Glu Arg Gln Phe Gly Pro Thr Phe Ala Leu Asp Thr Val His Val Asp  
100 105 110

Pro Val Ile Arg Glu Ser Thr Pro Asp Glu Leu Leu Arg Pro Pro Ala  
115 120 125

Glu Leu Ala Leu Glu His Gln Pro Pro Gln Ala Gly Leu Pro Pro Leu  
130 135 140

Ala Leu Ser Gln Leu Phe Asn Pro Asp Ala Cys Gly Arg Arg Val Gln  
145 150 155 160

Thr Val Val Leu Tyr Gly Thr Val Gly Thr Gly Lys Ser Thr Leu Val  
165 170 175

Arg Lys Met Val Leu Asp Trp Cys Tyr Gly Arg Leu Pro Ala Phe Glu  
180 185 190

Leu Leu Ile Pro Phe Ser Cys Glu Asp Leu Ser Ser Leu Gly Pro Ala  
195 200 205

Pro Ala Ser Leu Cys Gln Leu Val Ala Gln Arg Tyr Thr Pro Leu Lys  
210 215 220

Glu Val Leu Pro Leu Met Ala Ala Ala Gly Ser His Leu Leu Phe Val

225

230

235

240

Leu His Gly Leu Glu His Leu Asn Leu Asp Phe Arg Leu Ala Gly Thr  
245 250 255

Gly Leu Cys Ser Asp Pro Glu Glu Pro Gln Glu Pro Ala Ala Ile Ile  
260 265 270

Val Asn Leu Leu Arg Lys Tyr Met Leu Pro Gln Ala Ser Ile Leu Val  
275 280 285

Thr Thr Arg Pro Ser Ala Ile Gly Arg Ile Pro Ser Lys Tyr Val Gly  
290 295 300

Arg Tyr Gly Glu Ile Cys Gly Phe Ser Asp Thr Asn Leu Gln Lys Leu  
305 310 315 320

Tyr Phe Gln Leu Arg Leu Asn Gln Pro Tyr Cys Gly Tyr Ala Val Gly  
325 330 335

Gly Ser Gly Val Ser Ala Thr Pro Ala Gln Arg Asp His Leu Val Gln  
340 345 350

Met Leu Ser Arg Asn Leu Glu Gly His His Gln Ile Ala Ala Ala Cys  
355 360 365

Phe Leu Pro Ser Tyr Cys Trp Leu Val Cys Ala Thr Leu His Phe Leu  
370 375 380

His Ala Pro Thr Pro Ala Gly Gln Thr Leu Thr Ser Ile Tyr Thr Ser  
385 390 395 400

Phe Leu Arg Leu Asn Phe Ser Gly Glu Thr Leu Asp Ser Thr Asp Pro  
405 410 415

Ser Asn Leu Ser Leu Met Ala Tyr Ala Ala Arg Thr Met Gly Lys Leu  
420 425 430

Ala Tyr Glu Gly Val Ser Ser Arg Lys Thr Tyr Phe Ser Glu Glu Asp  
435 440 445

Val Cys Gly Cys Leu Glu Ala Gly Ile Arg Thr Glu Glu Glu Phe Gln  
450 455 460

Leu Leu His Ile Phe Arg Arg Asp Ala Leu Arg Phe Phe Leu Ala Pro  
465 470 475 480

Cys Val Glu Pro Gly Arg Ala Gly Thr Phe Val Phe Thr Val Pro Ala  
485 490 495

Met Gln Glu Tyr Leu Ala Ala Leu Tyr Ile Val Leu Gly Leu Arg Lys  
500 505 510

Thr Thr Leu Gln Lys Val Gly Lys Glu Val Ala Glu Leu Val Gly Arg  
515 520 525

Val Gly Glu Asp Val Ser Leu Val Leu Gly Ile Met Ala Lys Leu Leu  
530 535 540

Pro Leu Arg Ala Leu Pro Leu Leu Phe Asn Leu Ile Lys Val Val Pro  
545 550 555 560

Arg Val Phe Gly Arg Met Val Gly Lys Ser Arg Glu Ala Val Thr Gln  
565 570 575

Ala Met Val Leu Glu Met Phe Arg Glu Glu Asp Tyr Tyr Asn Asp Asp  
580 585 590

Val Leu Asp Gln Met Gly Ala Ser Ile Leu Gly Val Glu Gly Pro Arg  
595 600 605

Arg His Pro Asp Glu Pro Pro Glu Asp Glu Val Phe Glu Leu Phe Pro  
610 615 620

Met Phe Met Gly Gly Leu Leu Ser Ala His Asn Arg Ala Val Leu Ala  
625 630 635 640

Gln Leu Gly Cys Pro Ile Lys Asn Leu Asp Ala Leu Glu Asn Ala Gln  
645 650 655

Ala Ile Lys Lys Lys Leu Gly Lys Leu Gly Arg Gln Val Leu Pro Pro  
660 665 670

Ser Glu Leu Leu Asp His Leu Phe Phe His Tyr Glu Phe Gln Asn Gln  
675 680 685

Arg Phe Ser Ala Glu Val Leu Ser Ser Leu Arg Gln Leu Asn Leu Ala  
690 695 700

Gly Val Arg Met Thr Pro Val Lys Cys Thr Val Val Ala Ala Val Leu  
705 710 715 720

Gly Ser Gly Arg His Ala Leu Asp Glu Val Asn Leu Ala Ser Cys Gln  
725 730 735

Leu Asp Pro Ala Gly Leu Arg Thr Leu Leu Pro Val Phe Leu Arg Ala  
740 745 750

Arg Lys Leu Gly Leu Gln Leu Asn Ser Leu Gly Pro Glu Ala Cys Lys  
755 760 765

Asp Leu Arg Asp Leu Leu His Asp Gln Cys Gln Ile Thr Thr Leu  
770 775 780

Arg Leu Ser Asn Asn Pro Leu Thr Glu Ala Gly Val Ala Val Leu Met  
785 790 795 800

Glu Gly Leu Ala Gly Asn Thr Ser Val Thr His Leu Ser Leu Leu His  
805 810 815

Thr Gly Leu Gly Asp Glu Gly Leu Glu Leu Leu Ala Ala Gln Leu Asp  
820 825 830

Arg Asn Arg Gln Leu Gln Glu Leu Asn Val Ala Tyr Asn Gly Ala Gly  
835 840 845

Asp Thr Ala Ala Leu Ala Leu Ala Arg Ala Ala Arg Glu His Pro Ser  
850 855 860

Leu Glu Leu Leu Gln Gly Val Ala Ile Gln Met Cys Trp Lys Leu Pro  
865 870 875 880

Leu Leu Pro Tyr Ala His Leu Trp Thr Pro Arg Met Pro Ser His Trp  
885 890 895

Cys Phe Leu Leu Ile Leu Met Pro Pro Leu Pro Gln Trp Tyr Asp Gly  
900 905 910

Leu Val Ala Pro Arg Gly Arg Cys Thr Leu Ala Ala Ile Lys Lys Pro  
915 920 925

Cys Ala Phe Tyr  
930

<210> 21  
<211> 3464  
<212> DNA  
<213> Homo sapiens

<400>	21					
atgctgcaga	attttaagta	cccaaagttt	ctcaacaagt	tgattttcaa	gcaagctcac	60
cggttccccca	gctcatcttc	cttccagttc	ccctgtcccc	cagctcaact	gcctgcctc	120
agttcacctg	tcccccagtt	catcttcctc	ctagctcccc	tgtcccccag	ctcacctgtg	180
ccccagctcc	cctgtcccccc	aggctggctc	ctcatggacc	ccggtggcct	ccagctcgac	240
aacaagaacc	tgtggagctg	tcttgtgagg	ctgctcacca	aagacccaga	atggctgaac	300
gccaaagatga	agttcttcct	ccccaacacg	gacctggatt	ccaggaacga	gaccttggac	360
cctgaacaga	gagtcatcct	gcaactcaac	aagctgcatg	tccagggttc	ggacacactgg	420
cagtcttca	ttcattgtgt	gtgcatgcag	ctggagggtgc	ctctggacct	ggaggtgctg	480
ctgctgagta	cttttgcta	tgatgatggg	ttcaccagcc	agctgggagc	tgaggggaaa	540
agccaaacctg	aatctcagct	ccaccatggc	ctgaagcgcc	cacatcagag	ctgtgggtcc	600
tcaccccgcc	ggaaggcagtg	caagaagcag	cagctagagt	tggccaagaa	gtacctgcag	660
ctcctgcgga	cctctgccc	gcagcgctac	aggagccaaa	tccctgggtc	agggcagccc	720
cacgccttcc	accaggtcta	tgtccctcca	atcctgcgcc	ggcccacago	atccttagac	780
actccggagg	gggccattat	ggggacgtc	aaggtggaag	atggtgctga	cgtgagcatc	840
tcggacctct	tcaacaccag	ggttaacaag	ggcccggaggg	tgaccgtgct	tttgggaaag	900
gctggcatgg	gcaagaccac	gctggccac	cggctctgcc	agaagtgggc	agagggccat	960
ctgaactgtt	tccagggcct	gttcctttt	gaattccgcc	agctcaactt	gatcacgagg	1020
ttcctgacac	cgtccgagct	ccttttgat	ctgtacctga	gccctgaatc	ggaccacgac	1080
actgtottcc	agtacctgga	gaagaacgct	gaccaagtcc	tgctgatctt	tgatgggcta	1140
gatgaggccc	tccagcctat	gggtcctgat	ggcccagggcc	cagtcctcac	cctttctcc	1200
catctctgca	atgggaccct	cctgcctggc	tgccgggcag	ccatggtcca	catgttggc	1260
tttcatggc	cacgggtgga	agaatatgtg	aatcacttct	tcagcgccca	gccatcgccg	1320
gagggggccc	tggtgagtt	acagacaaat	ggacgtctcc	gaagcctgtg	tgcgggtccc	1380
gcactgtgcc	aagtgcgcctg	tctctgcctc	caccatctgc	ttcctgacca	cgccccaggc	1440
cagtctgtgg	ccctcctgcc	caacatgact	cagctctata	tgcagatgg	gctcgccctc	1500
agccccctg	ggcacttgcc	cacctcgatcc	ctactggacc	tgggggaggt	ggccctgagg	1560
ggccctggag	acagggaaagg	ccctgggcac	cagcagacag	gctatgcttt	cacccacctc	1620
agcctgcagg	agtttcttgc	tgcctgcac	ctgatggcca	gccccaaaggt	gaacaaagac	1680
acacttaccc	agtatgttac	cctccattcc	cgctgggtac	agcggaccaa	agctagactg	1740
ggcctctcag	accacccccc	cacccctctg	gcgggcctgg	catcctgcac	ctgcccffff	1800

ttecttagcc	acctggcgca	gggcaatgag	gactgtgtgg	gtgccaagca	ggctgctgtta	1860
gtgcagggtgt	tgaagaagtt	ggccacccgc	aagctcacag	ggccaaaggt	tgttagagctg	1920
tgtcactgtg	tggatgagac	acaggagcct	gagctggcca	gtctcaccgc	acaaaggcctc	1980
ccctatcaac	tgcgccttcca	caatttccc	ctgacctgca	ccgacctggc	caccctgacc	2040
aacatcctag	agcacaggg	ggcccccatc	cacctggatt	ttgatggctg	tcccctggag	2100
ccccactgcc	ctgaggctct	gttaggctgt	ggcagatag	agaatctcag	ctttaagagc	2160
aggaagtgtg	gggatgcctt	tgcagaagcc	ctctccagga	gcttgccgac	aatggggagg	2220
ctgcagatgc	tggggtagc	aggaagtaaa	atcaactgccc	gaggcatcag	ccacctggtg	2280
aaagctttgc	ctctctgtcc	acagctgaaa	gaagtcagtt	ttcgggacaa	ccagctcagt	2340
gaccaggtgg	tgctgaacat	tgtggaggtt	ctccctcacc	taccacggct	ccggaagctt	2400
gacctctcag	ggaaccagct	ggaagatgaa	ggctgtcgcc	tatggcaga	ggctgcaccc	2460
cagctgcaca	tcgcccaggaa	gctggacctc	agtaacaacg	ggctttctgt	ggccgggggt	2520
cattgtgtgc	tgagggccgt	gagtgcgtgc	tggaccctgg	cagagctgca	catcaggctg	2580
acacattgtg	gcctccaaga	aaagcaccta	gagcagctct	gcaaggctct	gggaggaagc	2640
tgccacctcg	gtcacctcca	cctcgacttc	tcaggcaatg	ctctggggga	tgaaggtgca	2700
gcccggctgg	ctcagctgct	cccagggctg	ggagctctgc	agtccctgaa	cctcagtgag	2760
aacggtttgt	ccctggatgc	cgtgttgggt	ttggttcggt	gcttctccac	tctgcagtgg	2820
ctcttccgct	tggacatcag	cctcagtgag	tgtcctctgg	agcccccaag	cctcaccggc	2880
ctctgtgcca	ctctgaagga	ctgcccggga	cccctggAAC	tgcaattgtc	ctgtgagttc	2940
ctgagtgacc	agagcctgga	gactctactg	gactgcttac	ctcaactccc	tcagctgagc	3000
ctgctgcagc	tgagccagac	gggactgtcc	ccgaaaaAGCC	ccttcctgct	ggccaacacc	3060
ttaagcctgt	gtccacgggt	taaaaaggtg	gatctcaggt	tcacaggctg	cagcctcagc	3120
caggagcagc	tagagtca	ctgctggtt	ctgagcaagt	gtaaagacct	cagccagggt	3180
gatctctcag	caaacctgct	gggcgacagc	ggactcagat	gccttctgga	atgtctgccc	3240
caggtgcccc	tctccggttt	gcttggagagc	ttggtcacgg	cctgtgggac	tgtgtcgccg	3300
atcgccggcc	gcaaccccca	atggccacccg	aagtgtgcc	tccgcgtgcg	atgggggaca	3360
ccgtgctgcg	ggctgtcggt	caggacatct	tatgtgggtt	attgcggcgc	caatacccg	3420
tcacccttat	tgcaggggg	gatatggcat	tctcctctat	gtgg		3464

<210> 22  
 <211> 1154  
 <212> PRT

<213> Homo sapiens

<400> 22

Met Leu Gln Asn Phe Lys Tyr Pro Lys Phe Leu Asn Lys Leu Ile Phe  
1 5 10 15

Lys Gln Ala His Arg Phe Pro Ser Ser Ser Phe Gln Phe Pro Cys  
20 25 30

Pro Pro Ala Gln Leu Pro Ala Leu Ser Ser Pro Val Pro Gln Phe Ile  
35 40 45

Phe Leu Leu Ala Pro Leu Ser Pro Ser Ser Pro Val Pro Gln Leu Pro  
50 55 60

Cys Pro Pro Gly Trp Leu Leu Met Asp Pro Val Gly Leu Gln Leu Gly  
65 70 75 80

Asn Lys Asn Leu Trp Ser Cys Leu Val Arg Leu Leu Thr Lys Asp Pro  
85 90 95

Glu Trp Leu Asn Ala Lys Met Lys Phe Phe Leu Pro Asn Thr Asp Leu  
100 105 110

Asp Ser Arg Asn Glu Thr Leu Asp Pro Glu Gln Arg Val Ile Leu Gln  
115 120 125

Leu Asn Lys Leu His Val Gln Gly Ser Asp Thr Trp Gln Ser Phe Ile  
130 135 140

His Cys Val Cys Met Gln Leu Glu Val Pro Leu Asp Leu Glu Val Leu  
145 150 155 160

Leu Leu Ser Thr Phe Gly Tyr Asp Asp Gly Phe Thr Ser Gln Leu Gly  
165 170 175

Ala Glu Gly Lys Ser Gln Pro Glu Ser Gln Leu His His Gly Leu Lys  
180 185 190

Arg Pro His Gln Ser Cys Gly Ser Ser Pro Arg Arg Lys Gln Cys Lys  
195 200 205

Lys Gln Gln Leu Glu Leu Ala Lys Lys Tyr Leu Gln Leu Leu Arg Thr  
210 215 220

Ser Ala Gln Gln Arg Tyr Arg Ser Gln Ile Pro Gly Ser Gly Gln Pro

225

230

235

240

His Ala Phe His Gln Val Tyr Val Pro Pro Ile Leu Arg Arg Ala Thr  
245 250 255

Ala Ser Leu Asp Thr Pro Glu Gly Ala Ile Met Gly Asp Val Lys Val  
260 265 270

Glu Asp Gly Ala Asp Val Ser Ile Ser Asp Leu Phe Asn Thr Arg Val  
275 280 285

Asn Lys Gly Pro Arg Val Thr Val Leu Leu Gly Lys Ala Gly Met Gly  
290 295 300

Lys Thr Thr Leu Ala His Arg Leu Cys Gln Lys Trp Ala Glu Gly His  
305 310 315 320

Leu Asn Cys Phe Gln Ala Leu Phe Leu Phe Glu Phe Arg Gln Leu Asn  
325 330 335

Leu Ile Thr Arg Phe Leu Thr Pro Ser Glu Leu Leu Phe Asp Leu Tyr  
340 345 350

Leu Ser Pro Glu Ser Asp His Asp Thr Val Phe Gln Tyr Leu Glu Lys  
355 360 365

Asn Ala Asp Gln Val Leu Ile Phe Asp Gly Leu Asp Glu Ala Leu  
370 375 380

Gln Pro Met Gly Pro Asp Gly Pro Gly Pro Val Leu Thr Leu Phe Ser  
385 390 395 400

His Leu Cys Asn Gly Thr Leu Leu Pro Gly Cys Arg Ala Ala Met Val  
405 410 415

His Met Leu Gly Phe Asp Gly Pro Arg Val Glu Glu Tyr Val Asn His  
420 425 430

Phe Phe Ser Ala Gln Pro Ser Arg Glu Gly Ala Leu Val Glu Leu Gln  
435 440 445

Thr Asn Gly Arg Leu Arg Ser Leu Cys Ala Val Pro Ala Leu Cys Gln  
450 455 460

Val Ala Cys Leu Cys Leu His His Leu Leu Pro Asp His Ala Pro Gly  
465 470 475 480

Gln Ser Val Ala Leu Leu Pro Asn Met Thr Gln Leu Tyr Met Gln Met  
485 490 495

Val Leu Ala Leu Ser Pro Pro Gly His Leu Pro Thr Ser Ser Leu Leu  
500 505 510

Asp Leu Gly Glu Val Ala Leu Arg Gly Pro Gly Asp Arg Glu Gly Pro  
515 520 525

Gly His Gln Gln Thr Gly Tyr Ala Phe Thr His Leu Ser Leu Gln Glu  
530 535 540

Phe Leu Ala Ala Leu His Leu Met Ala Ser Pro Lys Val Asn Lys Asp  
545 550 555 560

Thr Leu Thr Gln Tyr Val Thr Leu His Ser Arg Trp Val Gln Arg Thr  
565 570 575

Lys Ala Arg Leu Gly Leu Ser Asp His Leu Pro Thr Phe Leu Ala Gly  
580 585 590

Leu Ala Ser Cys Thr Cys Arg Pro Phe Leu Ser His Leu Ala Gln Gly  
595 600 605

Asn Glu Asp Cys Val Gly Ala Lys Gln Ala Ala Val Val Gln Val Leu  
610 615 620

Lys Lys Leu Ala Thr Arg Lys Leu Thr Gly Pro Lys Val Val Glu Leu  
625 630 635 640

Cys His Cys Val Asp Glu Thr Gln Glu Pro Glu Leu Ala Ser Leu Thr  
645 650 655

Ala Gln Ser Leu Pro Tyr Gln Leu Pro Phe His Asn Phe Pro Leu Thr  
660 665 670

Cys Thr Asp Leu Ala Thr Leu Thr Asn Ile Leu Glu His Arg Glu Ala  
675 680 685

Pro Ile His Leu Asp Phe Asp Gly Cys Pro Leu Glu Pro His Cys Pro  
690 695 700

Glu Ala Leu Val Gly Cys Gly Gln Ile Glu Asn Leu Ser Phe Lys Ser  
705 710 715 720

Arg Lys Cys Gly Asp Ala Phe Ala Glu Ala Leu Ser Arg Ser Leu Pro  
725 730 735

Thr Met Gly Arg Leu Gln Met Leu Gly Leu Ala Gly Ser Lys Ile Thr  
740 745 750

Ala Arg Gly Ile Ser His Leu Val Lys Ala Leu Pro Leu Cys Pro Gln  
755 760 765

Leu Lys Glu Val Ser Phe Arg Asp Asn Gln Leu Ser Asp Gln Val Val  
770 775 780

Leu Asn Ile Val Glu Val Leu Pro His Leu Pro Arg Leu Arg Lys Leu  
785 790 795 800

Asp Leu Ser Gly Asn Gln Leu Glu Asp Glu Gly Cys Arg Leu Met Ala  
805 810 815

Glu Ala Ala Ser Gln Leu His Ile Ala Arg Lys Leu Asp Leu Ser Asn  
820 825 830

Asn Gly Leu Ser Val Ala Gly Val His Cys Val Leu Arg Ala Val Ser  
835 840 845

Ala Cys Trp Thr Leu Ala Glu Leu His Ile Arg Leu Thr His Cys Gly  
850 855 860

Leu Gln Glu Lys His Leu Glu Gln Leu Cys Lys Ala Leu Gly Gly Ser  
865 870 875 880

Cys His Leu Gly His Leu His Leu Asp Phe Ser Gly Asn Ala Leu Gly  
885 890 895

Asp Glu Gly Ala Ala Arg Leu Ala Gln Leu Leu Pro Gly Leu Gly Ala  
900 905 910

Leu Gln Ser Leu Asn Leu Ser Glu Asn Gly Leu Ser Leu Asp Ala Val  
915 920 925

Leu Gly Leu Val Arg Cys Phe Ser Thr Leu Gln Trp Leu Phe Arg Leu  
930 935 940

Asp Ile Ser Leu Ser Glu Cys Pro Leu Glu Pro Pro Ser Leu Thr Arg  
945 950 955 960

Leu Cys Ala Thr Leu Lys Asp Cys Pro Gly Pro Leu Glu Leu Gln Leu  
965 970 975

Ser Cys Glu Phe Leu Ser Asp Gln Ser Leu Glu Thr Leu Leu Asp Cys  
980 985 990

Leu Pro Gln Leu Pro Gln Leu Ser Leu Leu Gln Leu Ser Gln Thr Gly  
995 1000 1005

Leu Ser Pro Lys Ser Pro Phe Leu Leu Ala Asn Thr Leu Ser Leu  
1010 1015 1020

Cys Pro Arg Val Lys Lys Val Asp Leu Arg Phe Thr Gly Cys Ser  
1025 1030 1035

Leu Ser Gln Glu His Val Glu Ser Leu Cys Trp Leu Leu Ser Lys  
1040 1045 1050

Cys Lys Asp Leu Ser Gln Val Asp Leu Ser Ala Asn Leu Leu Gly  
1055 1060 1065

Asp Ser Gly Leu Arg Cys Leu Leu Glu Cys Leu Pro Gln Val Pro  
1070 1075 1080

Ile Ser Gly Leu Leu Glu Ser Leu Val Thr Ala Cys Gly Thr Val  
1085 1090 1095

Ser Pro Ile Ala Pro Gly Asn Pro Gln Trp Pro Pro Lys Cys Ala  
1100 1105 1110

Ile Arg Val Arg Trp Gly Thr Pro Cys Cys Gly Leu Ser Phe Arg  
1115 1120 1125

Thr Ser Tyr Val Gly Tyr Cys Gly Ala Asn Thr Arg Ser Pro Leu  
1130 1135 1140

Leu Gln Gly Gly Ile Trp His Ser Pro Leu Cys  
1145 1150

<210> 23

<211> 4464

<212> DNA

<213> Homo sapiens

<400> 23

ggcccagtcc tcaccctttt ctccccatctc tgcaatggga ccctcctgcc tggctgccgg 60

gtgatggctca cctcccgatcc agggaaagctg cctgcctgcc tgcctgcaga ggcagccatg 120

gtccacatgt tgggcttga tgggccacgg gtggaaagaat atgtaatca cttttcagc	180
gcccagccat cgcgggagggg ggccctggtg gagttacaga caaatggacg tctccgaagc	240
ctgtgtgcgg tgcccgact gtgccaagtc gcctgtctct gcctccacca tctgcttcct	300
gaccacgccc caggccagtc tgtggccctc ctgccccaca tgactcagct ctatatgcag	360
atggtgctcg ccctcagccc ccctggcac ttgctcacct cgccctact ggacctgggg	420
gaggtggccc tgaggggcct ggagacaggg aaggttatct tctatgaaa agatattgct	480
ccacccttga tagtttgg ggccactcac agcctgctga cttccctctg cgtccgcaca	540
ggccctggc accagcagac aggctatgct ttcacccacc tcagcctgca ggagttctt	600
gctgcctgc acctgatggc cagccccaaag gtgaacaaag acacacttac ccagtatgtt	660
accctccatt cccgctgggt acagcggacc aaagctagac tggccctctc agaccacctc	720
cccaccccttcc tggcgggcct ggcattcctgc acctgcccgc cttcccttag ccacctggcg	780
cagggcaatg aggactgtgt gggtgccaaag caggctgctg tagtgcaggt gttgaagaag	840
ttggccaccc gcaagctcac agggccaaag gttgttagagc tgggtcaactg tggatgag	900
acacaggagc ctgagctggc cagtcacc gcacaaagcc tcccttatca actgccttc	960
cacaatttcc cactgacctg caccgacctg gccaccctga ccaacatcct agagcacagg	1020
gaggccccca tccacctgga ttttgcgttgc tggccctgg agccccactg ccctgaggct	1080
ctggtaggct gtgggcagat agagaatctc agcttaaga gcaggaagtg tggatgcc	1140
tttgcagaag ccctctccag gagctgccc acaatggggaa ggctgcagat gctgggtta	1200
gcaggaagta aaatcactgc ccgaggcatc agccacctgg taaaagctt gcctctctgt	1260
ccacagctga aagaagtcag tttcgggac aaccagctca gtgaccaggt ggtgctgaac	1320
attgtggagg ttctccctca cttaccacgg ctccggaaagc ttgacctgag cagcaacagc	1380
atctgcgtgt caaccctact ctgcttggca agggtggcag tcaacgtgtcc taccgtcagg	1440
atgcttcagg ccagggagcg gaccatcatc ttcccttcccccac agagacaact	1500
gcagagctac aaagagctcc agacctgcag gaaagtgcacg gccagaggaa aggggctcag	1560
agcagaagct tgacgctcag gctgcagaag tggcagctcc aggtccacga tggggaggcc	1620
ctcatagccc tgctccagga aggccctcac ctggaggaag tggacctctc agggaaaccag	1680
ctggaagatg aaggctgtcg gctgatggca gaggctgcac cccagctgca catgcccagg	1740
aagctggacc tcagcgacaa cgggcttct gtggccgggg tgcattgtgt gctgagggcc	1800
tgagtgcggt gctggaccct ggcagagctg cacatcagcc tgcagcaca aactgtgatc	1860
ttcatgtttg cccaggagcc agaggagcag aaggggccccc aggagagggc tgcatttctt	1920

gacagcctca	tgctccagat	gccctctgag	ctgcctctga	gctcccgaag	gatgagggctg	1980
acacattgtg	gcctccaaga	aaagcaccta	gagcagctct	gcaaggctct	gggaggaagc	2040
tgccacacctg	gtcacacctca	cctcgacttc	tcaggcaatg	ctctggggga	tgaaggtgca	2100
gccccggctgg	ctcagctgct	cccagggctg	ggagctctgc	agtccctgaa	cctcagtgag	2160
aacggtttgt	ccctggatgc	cgtgttgggc	ttggttcggt	gcttctccac	tctgcagtgg	2220
ctcttccgct	tggacatcag	cttgaaaagc	caacacatcc	tcctgagagg	ggacaagaca	2280
agcagcctca	gtgagtgccc	tctggagccc	ccaagcctca	ccgcctctg	tgccactctg	2340
aaggactgcc	cgggaccct	ggaactgcaa	ttgtcctgtg	agttcctgag	tgaccagagc	2400
ctggagactc	tactggactg	cttacctcaa	ctccctcagc	tgagcctgct	gcagctgagc	2460
cagacgggac	tgtccccgaa	aagcccttc	ctgctggcca	acacctaag	cctgtgtcca	2520
cgggttaaaa	aggtggatct	caggtccctg	caccatgcaa	cttgcactt	cagatccaac	2580
gaggaggagg	aaggcgtgtg	ctgtggcagg	ttcacaggct	gcagcctcag	ccaggagcac	2640
gtagagtcac	tctgctggtt	gctgagcaag	tgtaaagacc	tcagccaggt	ggatctgagt	2700
cacaacagca	tttctcagga	aagtgcctg	tacctgctgg	agacactgcc	ctcctgccc	2760
cgtgtccggg	aggcctcagt	gaacctggc	tctgagcaga	gctccggat	tcacttctcc	2820
agagaggacc	aggctggaa	gacactcagg	ctaagtgagt	gcagcttccg	gccagagcac	2880
gtgtccaggg	tggccaccgg	cttgagcaag	tccctgcagc	tgacggagct	cacgctgacc	2940
cagtgctgcc	tggccagaa	gcagctggcc	atcctcctga	gcttggtggg	gcgacccgca	3000
gggctgttca	gcctcagggt	gcaggagccg	tggcggaca	gagccagggt	tctctccctg	3060
ttagaagtct	gcgcccaggc	ctcaggcagt	gtcactgaaa	tcagcatctc	cgagacccag	3120
cagcagctct	gtgtccagct	ggaatttct	cgcaggaaag	agaatccaga	agctgtggca	3180
ctcaggttgg	ctcaactgtga	cttggagcc	caccacagcc	ttcttgcgg	gcagctgatg	3240
gagacatgtg	ccaggctgca	gcagctcagc	ttgtctcagg	ttaacctctg	tgaggacgt	3300
gatgccagtt	ccctgctgct	gcagagcctc	ctgctgtccc	tctctgagct	gaagacattt	3360
cggctgacct	ccagctgtgt	gagcaccgag	ggcctcgccc	acctggcatc	ttgtctggc	3420
cactgccacc	acttggagga	gctggacttg	tctaacaatc	aatttcatgt	ggagggcacc	3480
aaggcgctga	tgagggccct	tgagggaaa	tggatgctaa	agaggctgga	cctcagtcac	3540
cttctgctga	acagctccac	cttggccttg	cttactcaca	gactaagcca	gatgacctgc	3600
ctgcagagcc	tcagactgaa	caggaacagt	atcggtatg	tcggttgctg	ccaccttct	3660
gaggctctca	gggctgccac	cagcctagag	gagctggact	tgagccacaa	ccagattgga	3720
gacgctggtg	tcacgactt	agctaccatc	ctgcctgggc	tgccagagct	caggaagata	3780

gacctctcag ggaatagcat cagctcagcc gggggagtgc agttggcaga gtctctcgaa	3840
cttgcaggc gcctggagga gttgtatgctt ggctgcaatg ccctggggga tcccacagcc	3900
ctggggctgg ctcaggagct gccccagcac ctgagggtcc tacacctacc attcagccat	3960
ctgggcccag gtggggccct gagcctggcc caggccctgg atggatcccc ccatttgaa	4020
gagatcagct tggcggaaaa caacctggct ggaggggtcc tgcgtttctg tatggagctc	4080
ccgctgctca gacagataga cctggtttcc tgtaagattg acaaccagac tgccaagctc	4140
ctcacctcca gcttcacgag ctgccctgcc ctggaagtaa tcttgctgtc ctggaatctc	4200
ctcggggatg aggcagctgc cgagctggcc caggtgctgc cgaagatggg ccggctgaag	4260
agagtggacc tggagaagaa tcagatcaca gctttggggg cctggctcct ggctgaagga	4320
ctggcccagg ggtcttagcat ccaagtcata cgcctctgga ataacccat tccctgac	4380
atggcccagc acctgaagag ccaggagccc aggctggact ttgccttctt tgacaaccag	4440
cccccaqqccc cttggggatcac ttqa	4464

<210> 24  
<211> 1487  
<212> PRT  
<213> Homo sapiens  
  
<400> 24

Gly Pro Val Leu Thr Leu Phe Ser His Leu Cys Asn Gly Thr Leu Leu  
1 5 10 15

Pro Gly Cys Arg Val Met Ala Thr Ser Arg Pro Gly Lys Leu Pro Ala  
20 25 30

Cys Leu Pro Ala Glu Ala Ala Met Val His Met Leu Gly Phe Asp Gly  
35 40 45

Pro Arg Val Glu Glu Tyr Val Asn His Phe Phe Ser Ala Gln Pro Ser  
50 55 60

Arg Glu Gly Ala Leu Val Glu Leu Gln Thr Asn Gly Arg Leu Arg Ser  
65 70 75 80

Leu Cys Ala Val Pro Ala Leu Cys Gln Val Ala Cys Leu Cys Leu His  
85 90 95

His Leu Leu Pro Asp His Ala Pro Gly Gln Ser Val Ala Leu Leu Pro  
100 105 110

Asn Met Thr Gln Leu Tyr Met Gln Met Val Leu Ala Leu Ser Pro Pro  
115 120 125

Gly His Leu Leu Thr Ser Ser Leu Leu Asp Leu Gly Glu Val Ala Leu  
130 135 140

Arg Gly Leu Glu Thr Gly Lys Val Ile Phe Tyr Ala Lys Asp Ile Ala  
145 150 155 160

Pro Pro Leu Ile Ala Phe Gly Ala Thr His Ser Leu Leu Thr Ser Phe  
165 170 175

Arg Val Cys Thr Gly Pro Gly His Gln Gln Thr Gly Tyr Ala Phe Thr  
180 185 190

His Leu Ser Leu Gln Glu Phe Leu Ala Ala Leu His Leu Met Ala Ser  
195 200 205

Pro Lys Val Asn Lys Asp Thr Leu Thr Gln Tyr Val Thr Leu His Ser  
210 215 220

Arg Trp Val Gln Arg Thr Lys Ala Arg Leu Gly Leu Ser Asp His Leu  
225 230 235 240

Pro Thr Phe Leu Ala Gly Leu Ala Ser Cys Thr Cys Arg Pro Phe Leu  
245 250 255

Ser His Leu Ala Gln Gly Asn Glu Asp Cys Val Gly Ala Lys Gln Ala  
260 265 270

Ala Val Val Gln Val Leu Lys Lys Leu Ala Thr Arg Lys Leu Thr Gly  
275 280 285

Pro Lys Val Val Glu Leu Cys His Cys Val Asp Glu Thr Gln Glu Pro  
290 295 300

Glu Leu Ala Ser Leu Thr Ala Gln Ser Leu Pro Tyr Gln Leu Pro Phe  
305 310 315 320

His Asn Phe Pro Leu Thr Cys Thr Asp Leu Ala Thr Leu Thr Asn Ile  
325 330 335

Leu Glu His Arg Glu Ala Pro Ile His Leu Asp Phe Asp Gly Cys Pro  
340 345 350

Leu Glu Pro His Cys Pro Glu Ala Leu Val Gly Cys Gly Gln Ile Glu

355

360

365

Asn Leu Ser Phe Lys Ser Arg Lys Cys Gly Asp Ala Phe Ala Glu Ala  
370 375 380

Leu Ser Arg Ser Leu Pro Thr Met Gly Arg Leu Gln Met Leu Gly Leu  
385 390 395 400

Ala Gly Ser Lys Ile Thr Ala Arg Gly Ile Ser His Leu Val Lys Ala  
405 410 415

Leu Pro Leu Cys Pro Gln Leu Lys Glu Val Ser Phe Arg Asp Asn Gln  
420 425 430

Leu Ser Asp Gln Val Val Leu Asn Ile Val Glu Val Leu Pro His Leu  
435 440 445

Pro Arg Leu Arg Lys Leu Asp Leu Ser Ser Asn Ser Ile Cys Val Ser  
450 455 460

Thr Leu Leu Cys Leu Ala Arg Val Ala Val Thr Cys Pro Thr Val Arg  
465 470 475 480

Met Leu Gln Ala Arg Glu Arg Thr Ile Ile Phe Leu Leu Ser Pro Pro  
485 490 495

Thr Glu Thr Thr Ala Glu Leu Gln Arg Ala Pro Asp Leu Gln Glu Ser  
500 505 510

Asp Gly Gln Arg Lys Gly Ala Gln Ser Arg Ser Leu Thr Leu Arg Leu  
515 520 525

Gln Lys Cys Gln Leu Gln Val His Asp Ala Glu Ala Leu Ile Ala Leu  
530 535 540

Leu Gln Glu Gly Pro His Leu Glu Glu Val Asp Leu Ser Gly Asn Gln  
545 550 555 560

Leu Glu Asp Glu Gly Cys Arg Leu Met Ala Glu Ala Ala Ser Gln Leu  
565 570 575

His Ile Ala Arg Lys Leu Asp Leu Ser Asp Asn Gly Leu Ser Val Ala  
580 585 590

Gly Val His Cys Val Leu Arg Ala Val Ser Ala Cys Trp Thr Leu Ala  
595 600 605

Glu Leu His Ile Ser Leu Gln His Lys Thr Val Ile Phe Met Phe Ala  
610 615 620

Gln Glu Pro Glu Glu Gln Lys Gly Pro Gln Glu Arg Ala Ala Phe Leu  
625 630 635 640

Asp Ser Leu Met Leu Gln Met Pro Ser Glu Leu Pro Leu Ser Ser Arg  
645 650 655

Arg Met Arg Leu Thr His Cys Gly Leu Gln Glu Lys His Leu Glu Gln  
660 665 670

Leu Cys Lys Ala Leu Gly Gly Ser Cys His Leu Gly His Leu His Leu  
675 680 685

Asp Phe Ser Gly Asn Ala Leu Gly Asp Glu Gly Ala Ala Arg Leu Ala  
690 695 700

Gln Leu Leu Pro Gly Leu Gly Ala Leu Gln Ser Leu Asn Leu Ser Glu  
705 710 715 720

Asn Gly Leu Ser Leu Asp Ala Val Leu Gly Leu Val Arg Cys Phe Ser  
725 730 735

Thr Leu Gln Trp Leu Phe Arg Leu Asp Ile Ser Phe Glu Ser Gln His  
740 745 750

Ile Leu Leu Arg Gly Asp Lys Thr Ser Ser Leu Ser Glu Cys Pro Leu  
755 760 765

Glu Pro Pro Ser Leu Thr Arg Leu Cys Ala Thr Leu Lys Asp Cys Pro  
770 775 780

Gly Pro Leu Glu Leu Gln Leu Ser Cys Glu Phe Leu Ser Asp Gln Ser  
785 790 795 800

Leu Glu Thr Leu Leu Asp Cys Leu Pro Gln Leu Pro Gln Leu Ser Leu  
805 810 815

Leu Gln Leu Ser Gln Thr Gly Leu Ser Pro Lys Ser Pro Phe Leu Leu  
820 825 830

Ala Asn Thr Leu Ser Leu Cys Pro Arg Val Lys Lys Val Asp Leu Arg  
835 840 845

Ser Leu His His Ala Thr Leu His Phe Arg Ser Asn Glu Glu Glu  
850 855 860

Gly Val Cys Cys Gly Arg Phe Thr Gly Cys Ser Leu Ser Gln Glu His  
865 870 875 880

Val Glu Ser Leu Cys Trp Leu Leu Ser Lys Cys Lys Asp Leu Ser Gln  
885 890 895

Val Asp Leu Ser His Asn Ser Ile Ser Gln Glu Ser Ala Leu Tyr Leu  
900 905 910

Leu Glu Thr Leu Pro Ser Cys Pro Arg Val Arg Glu Ala Ser Val Asn  
915 920 925

Leu Gly Ser Glu Gln Ser Phe Arg Ile His Phe Ser Arg Glu Asp Gln  
930 935 940

Ala Gly Lys Thr Leu Arg Leu Ser Glu Cys Ser Phe Arg Pro Glu His  
945 950 955 960

Val Ser Arg Leu Ala Thr Gly Leu Ser Lys Ser Leu Gln Leu Thr Glu  
965 970 975

Leu Thr Leu Thr Gln Cys Cys Leu Gly Gln Lys Gln Leu Ala Ile Leu  
980 985 990

Leu Ser Leu Val Gly Arg Pro Ala Gly Leu Phe Ser Leu Arg Val Gln  
995 1000 1005

Glu Pro Trp Ala Asp Arg Ala Arg Val Leu Ser Leu Leu Glu Val  
1010 1015 1020

Cys Ala Gln Ala Ser Gly Ser Val Thr Glu Ile Ser Ile Ser Glu  
1025 1030 1035

Thr Gln Gln Gln Leu Cys Val Gln Leu Glu Phe Pro Arg Gln Glu  
1040 1045 1050

Glu Asn Pro Glu Ala Val Ala Leu Arg Leu Ala His Cys Asp Leu  
1055 1060 1065

Gly Ala His His Ser Leu Leu Val Gly Gln Leu Met Glu Thr Cys  
1070 1075 1080

Ala Arg Leu Gln Gln Leu Ser Leu Ser Gln Val Asn Leu Cys Glu  
1085 1090 1095

Asp Asp Asp Ala Ser Ser Leu Leu Leu Gln Ser Leu Leu Leu Ser  
1100 1105 1110

Leu Ser Glu Leu Lys Thr Phe Arg Leu Thr Ser Ser Cys Val Ser  
1115 1120 1125

Thr Glu Gly Leu Ala His Leu Ala Ser Gly Leu Gly His Cys His  
1130 1135 1140

His Leu Glu Glu Leu Asp Leu Ser Asn Asn Gln Phe Asp Glu Glu  
1145 1150 1155

Gly Thr Lys Ala Leu Met Arg Ala Leu Glu Gly Lys Trp Met Leu  
1160 1165 1170

Lys Arg Leu Asp Leu Ser His Leu Leu Leu Asn Ser Ser Thr Leu  
1175 1180 1185

Ala Leu Leu Thr His Arg Leu Ser Gln Met Thr Cys Leu Gln Ser  
1190 1195 1200

Leu Arg Leu Asn Arg Asn Ser Ile Gly Asp Val Gly Cys Cys His  
1205 1210 1215

Leu Ser Glu Ala Leu Arg Ala Ala Thr Ser Leu Glu Glu Leu Asp  
1220 1225 1230

Leu Ser His Asn Gln Ile Gly Asp Ala Gly Val Gln His Leu Ala  
1235 1240 1245

Thr Ile Leu Pro Gly Leu Pro Glu Leu Arg Lys Ile Asp Leu Ser  
1250 1255 1260

Gly Asn Ser Ile Ser Ser Ala Gly Gly Val Gln Leu Ala Glu Ser  
1265 1270 1275

Leu Val Leu Cys Arg Arg Leu Glu Glu Leu Met Leu Gly Cys Asn  
1280 1285 1290

Ala Leu Gly Asp Pro Thr Ala Leu Gly Leu Ala Gln Glu Leu Pro  
1295 1300 1305

Gln His Leu Arg Val Leu His Leu Pro Phe Ser His Leu Gly Pro

1310

1315

1320

Gly Gly Ala Leu Ser Leu Ala Gln Ala Leu Asp Gly Ser Pro His  
1325 1330 1335

Leu Glu Glu Ile Ser Leu Ala Glu Asn Asn Leu Ala Gly Gly Val  
1340 1345 1350

Leu Arg Phe Cys Met Glu Leu Pro Leu Leu Arg Gln Ile Asp Leu  
1355 1360 1365

Val Ser Cys Lys Ile Asp Asn Gln Thr Ala Lys Leu Leu Thr Ser  
1370 1375 1380

Ser Phe Thr Ser Cys Pro Ala Leu Glu Val Ile Leu Leu Ser Trp  
1385 1390 1395

Asn Leu Leu Gly Asp Glu Ala Ala Ala Glu Leu Ala Gln Val Leu  
1400 1405 1410

Pro Lys Met Gly Arg Leu Lys Arg Val Asp Leu Glu Lys Asn Gln  
1415 1420 1425

Ile Thr Ala Leu Gly Ala Trp Leu Leu Ala Glu Gly Leu Ala Gln  
1430 1435 1440

Gly Ser Ser Ile Gln Val Ile Arg Leu Trp Asn Asn Pro Ile Pro  
1445 1450 1455

Cys Asp Met Ala Gln His Leu Lys Ser Gln Glu Pro Arg Leu Asp  
1460 1465 1470

Phe Ala Phe Phe Asp Asn Gln Pro Gln Ala Pro Trp Gly Thr  
1475 1480 1485

<210> 25  
<211> 2230  
<212> DNA  
<213> Homo sapiens

<400> 25  
atgaggaagc aagaggtgcg gacgggcagg gaggccggcc agggccacgg tacggctcc 60  
ccagccgagc aggtgaaagc cctcatggat ctgctggctg ggaagggcag tcaaggctcc 120  
caggccccgc aggccctgga taggacaccg gatgccccgc tggggccctg cagcaatgac 180  
tcaaggatac agaggcacccg caaggccctg ctgagcaagg tgggaggtgg cccggagctg 240

ggcggaccct ggcacaggct ggcctccctc ctgctggtgg agggcctgac ggacctgcag	300
ctgagggAAC acgacttcac acaggtggag gccacccgcg ggggcgggca ccccgccagg	360
accgtcgccc tggaccggct cttcctgcct ctctcccggt tgtctgtccc accccgggtc	420
tccatcacta tcggggtgtgc cggtcatgggc aagaccaccc tggtgaggca cttcgccgc	480
ctctgggccc atgggcaggt cggcaaggac ttctcgctgg tgctgcctct gaccttccgg	540
gatctcaaca cccacgagaa gctgtgtgcc gaccgactca tctgctcggt cttccgcac	600
gtcggggagc ccagcctggc ggtggcagtc ccagccaggg ccctcctgat cctggacggc	660
ttggatgagt gcaggacgccc tctggacttc tccaacaccc tggcctgcac ggacccaaag	720
aaggagatcc cgggtggacca cctgatcacc aacatcatcc gtggcaacccct cttccggaa	780
gtttccatct ggatcacctc ccgtcccagt gcatctggcc agatcccagg gggcctggtg	840
gaccggatga cggagatccg gggcttaac gaggaggaga tcaaggtgtg tttggagcag	900
atgttccccg aggaccaggc cttctgggc tggatgctga gccaagtgca ggctgacagg	960
gccctgtacc tcatgtgcac cgtcccagcc ttctgcaggg tcacggggat ggctgcttaggc	1020
cacctgtggc gcagcaggac gggggcccccag gatgcagagc tggggccccc gaggaccctg	1080
tgcgagctct actcatggta cttaggatg gcccctcagcg gggaggggca ggagaaggc	1140
aaggcaagcc ctcgcacatcgac gcagggtggcc catgggtggcc gcaagatggt gggacattg	1200
ggccgtctgg cttccatgg gctgctcaag aagaaatacg tggggccccc gaggaccctg	1260
aaggcgtttgg tggtagaccc ctgtctgctg cagggcgccc cgtgcagctg ctgcctgcag	1320
agagaggaga cgttggcatc gtcagtggcc tactgcttca cccacctgtc cctgcaggag	1380
tttgcgttgcag ccgcgttata ctatggcgca tccaggaggg ccatcttcga cctcttca	1440
gagagcggcg tatcctggcc caggctggc ttcctcacgc atttcaggag cgccagccag	1500
cgggcacatgc aggcagagga cggggaggctg gacgtgttcc tgcgtttccct ctccggcctc	1560
ttgtctccga gggtaatgc ctcctggcc ggctccctgc tggcccaagg cgagcaccag	1620
gcctaccgga cccaggtggc tgagctcctg cagggctgcc tgcggccccc tgccgcagtc	1680
tgtgcacggg ccatcaacgt gttgcactgc ctgcacatcg tgcaacacac cgagctggcc	1740
cgcagcgtgg aggaggccat ggagagcggg gcccctggcca ggctgactgg tcccggcgcac	1800
cgcgcgtccc tggcctaccc ctcgcagggtg tccgcacgcgt gtgcccagga ggccaaacctg	1860
tccctgagcc tcagccaggc cgtccttcag agcctgctgc cccagctgct ctactgcccgg	1920
aagctcaggc tgcgttactt cagtcctcc cgtgcctgg tcatcttctc cctgtgtctg	1980
tctccacatg gtgctgtctt ctctttttt ttgagatgga gtcttgctct gtcggccagg	2040
ctggaataaca gtggcgccat ctcagctcac tgcaaacgct gcctcctggg ttcaagcgat	2100

tctcctgcct cagcctccct agtagctggg attacagggtg cccgccatca tgccctggcta 2160  
atttttgtgt ttttagtaga gacggggttt caccatgttgc ccaggctgc tctcaaactc 2220  
ctgacctcag 2230

<210> 26  
<211> 743  
<212> PRT  
<213> Homo sapiens

<400> 26

Met Arg Lys Gln Glu Val Arg Thr Gly Arg Glu Ala Gly Gln Gly His  
1 5 10 15

Gly Thr Gly Ser Pro Ala Glu Gln Val Lys Ala Leu Met Asp Leu Leu  
20 25 30

Ala Gly Lys Gly Ser Gln Gly Ser Gln Ala Pro Gln Ala Leu Asp Arg  
35 40 45

Thr Pro Asp Ala Pro Leu Gly Pro Cys Ser Asn Asp Ser Arg Ile Gln  
50 55 60

Arg His Arg Lys Ala Leu Leu Ser Lys Val Gly Gly Pro Glu Leu  
65 70 75 80

Gly Gly Pro Trp His Arg Leu Ala Ser Leu Leu Leu Val Glu Gly Leu  
85 90 95

Thr Asp Leu Gln Leu Arg Glu His Asp Phe Thr Gln Val Glu Ala Thr  
100 105 110

Arg Gly Gly Gly His Pro Ala Arg Thr Val Ala Leu Asp Arg Leu Phe  
115 120 125

Leu Pro Leu Ser Arg Val Ser Val Pro Pro Arg Val Ser Ile Thr Ile  
130 135 140

Gly Val Ala Gly Met Gly Lys Thr Thr Leu Val Arg His Phe Val Arg  
145 150 155 160

Leu Trp Ala His Gly Gln Val Gly Lys Asp Phe Ser Leu Val Leu Pro  
165 170 175

Leu Thr Phe Arg Asp Leu Asn Thr His Glu Lys Leu Cys Ala Asp Arg  
180 185 190

Leu Ile Cys Ser Val Phe Pro His Val Gly Glu Pro Ser Leu Ala Val  
195 200 205

Ala Val Pro Ala Arg Ala Leu Leu Ile Leu Asp Gly Leu Asp Glu Cys  
210 215 220

Arg Thr Pro Leu Asp Phe Ser Asn Thr Val Ala Cys Thr Asp Pro Lys  
225 230 235 240

Lys Glu Ile Pro Val Asp His Leu Ile Thr Asn Ile Ile Arg Gly Asn  
245 250 255

Leu Phe Pro Glu Val Ser Ile Trp Ile Thr Ser Arg Pro Ser Ala Ser  
260 265 270

Gly Gln Ile Pro Gly Gly Leu Val Asp Arg Met Thr Glu Ile Arg Gly  
275 280 285

Phe Asn Glu Glu Ile Lys Val Cys Leu Glu Gln Met Phe Pro Glu  
290 295 300

Asp Gln Ala Leu Leu Gly Trp Met Leu Ser Gln Val Gln Ala Asp Arg  
305 310 315 320

Ala Leu Tyr Leu Met Cys Thr Val Pro Ala Phe Cys Arg Leu Thr Gly  
325 330 335

Met Ala Leu Gly His Leu Trp Arg Ser Arg Thr Gly Pro Gln Asp Ala  
340 345 350

Glu Leu Trp Pro Pro Arg Thr Leu Cys Glu Leu Tyr Ser Trp Tyr Phe  
355 360 365

Arg Met Ala Leu Ser Gly Glu Gly Gln Glu Lys Gly Lys Ala Ser Pro  
370 375 380

Arg Ile Glu Gln Val Ala His Gly Gly Arg Lys Met Val Gly Thr Leu  
385 390 395 400

Gly Arg Leu Ala Phe His Gly Leu Leu Lys Lys Lys Tyr Val Phe Tyr  
405 410 415

Glu Gln Asp Met Lys Ala Phe Gly Val Asp Leu Ala Leu Leu Gln Gly  
420 425 430

Ala Pro Cys Ser Cys Phe Leu Gln Arg Glu Glu Thr Leu Ala Ser Ser  
435 440 445

Val Ala Tyr Cys Phe Thr His Leu Ser Leu Gln Glu Phe Val Ala Ala  
450 455 460

Ala Tyr Tyr Tyr Gly Ala Ser Arg Arg Ala Ile Phe Asp Leu Phe Thr  
465 470 475 480

Glu Ser Gly Val Ser Trp Pro Arg Leu Gly Phe Leu Thr His Phe Arg  
485 490 495

Ser Ala Ala Gln Arg Ala Met Gln Ala Glu Asp Gly Arg Leu Asp Val  
500 505 510

Phe Leu Arg Phe Leu Ser Gly Leu Leu Ser Pro Arg Val Asn Ala Leu  
515 520 525

Leu Ala Gly Ser Leu Leu Ala Gln Gly Glu His Gln Ala Tyr Arg Thr  
530 535 540

Gln Val Ala Glu Leu Leu Gln Gly Cys Leu Arg Pro Asp Ala Ala Val  
545 550 555 560

Cys Ala Arg Ala Ile Asn Val Leu His Cys Leu His Glu Leu Gln His  
565 570 575

Thr Glu Leu Ala Arg Ser Val Glu Glu Ala Met Glu Ser Gly Ala Leu  
580 585 590

Ala Arg Leu Thr Gly Pro Ala His Arg Ala Ala Leu Ala Tyr Leu Leu  
595 600 605

Gln Val Ser Asp Ala Cys Ala Gln Glu Ala Asn Leu Ser Leu Ser Leu  
610 615 620

Ser Gln Gly Val Leu Gln Ser Leu Leu Pro Gln Leu Leu Tyr Cys Arg  
625 630 635 640

Lys Leu Arg Leu Arg Tyr Phe Ser Leu Ser Arg Arg Leu Val Ile Phe  
645 650 655

Ser Leu Cys Leu Ser Pro His Gly Ala Val Leu Ser Phe Phe Leu Arg  
660 665 670

Trp Ser Leu Ala Leu Ser Pro Arg Leu Glu Tyr Ser Gly Ala Ile Ser  
675 680 685

Ala His Cys Lys Arg Cys Leu Leu Gly Ser Ser Asp Ser Pro Ala Ser  
690 695 700

Ala Ser Leu Val Ala Gly Ile Thr Gly Ala Arg His His Ala Trp Leu  
705 710 715 720

Ile Phe Val Phe Leu Val Glu Thr Gly Phe His His Val Gly Gln Ala  
725 730 735

Ala Leu Lys Leu Leu Thr Ser  
740

<210> 27  
<211> 3489  
<212> DNA  
<213> Homo sapiens

<400> 27  
atccccaggg catctaccac cacgcagctg gagcagggtc gagccca gcatggat 60  
ggacgc cccca aggccccca gtcttgctgt ccctggagca gcatcgaggc cggggagaac 120  
tgtggacaac ggaaggctga gccccatcca ttgagttcct gggcccccac tggagggct 180  
gctgtggcca gggtgcacgg tcacaaatga agacaccaag ggcgcagagag gtgactcagc 240  
ctgccctcag tcacctatct gtcctggag gtgatccccg actccatgag gaagcaagag 300  
gtgcggacgg gcaggaggc cggccaggc cacggta cgg gctccccagc cgaggcagg 360  
aaagccctca tggatctgct ggctggaa ggcagtcaag gctcccaggc cccgcaggcc 420  
ctggatagga caccggatgc cccgctggg ccctgcagca atgactcaag gatacagagg 480  
caccgcaagg ccctgctgag caagg tgg ggtggcccg agotggccgg accctggcac 540  
aggctggcct ccctcctgct ggtggaggc ctgacggacc tgcagctgag ggaacacgac 600  
ttcacacagg tggaggccac cggcggggc gggcacc ccaaggaccgt cggccctggac 660  
cggctcttcc tgcctcttc cgggtgtct gtcccaccc ggtctccat cactatcggg 720  
gtggccggca tggcaagac caccctggta aggcacttcg tccgcctctg gcccattgg 780  
caggtcggca aggacttctc gctggtgctg cctctgacct tccggatct caacacccac 840  
gagaagctgt gtgcccaccg actcatctgc tcggcttcc cgcacgtcgg ggagccacc 900  
ctggccggc cagttccacc caggccctc ctgatcctgg acggcttggta tgagtgcagg 960  
acgcctctgg acttctccaa caccgtggcc tgcacggacc caaagaagga gatcccggt 1020  
gaccacctga tcaccaacat catccgtggc aacctcttc cggaaagttc catctggatc 1080

acctcccgtc ccagtgcata tggccagatc ccagggggcc tggtgaccg gatgacggag	1140
atccggggct ttaacgagga ggagatcaag gtgttttg agcagatgtt ccccaggac	1200
caggcccttc tgggctggat gctgagccaa gtgcaggctg acagggccct gtacctgatg	1260
tgcacccgtcc cagccttctg caggctcacg gggatggcgc taggccacct gtggcgcagc	1320
aggacggggc cccaggatgc agagctgtgg ccccccggaga ccctgtgcga gctctactca	1380
tggtaactta gnatggccct cagcggggag gggcaggaga agggcaaggc aagccctcgc	1440
atcgagcagg tggcccatgg tggccgcaag atggtgggga cattgggccc tctggccttc	1500
catggctgc tcaagaagaa atacgtgttt tacgagcaag acatgaaggc gtttggtgta	1560
gacctcgctc tgctgcaggg cgccccgtgc agctgctcc tgcagagaga ggagacgttg	1620
gcatcgctcag tggcctactg ctacccac ctgtccctgc aggagttgt ggcagccgc	1680
tattactatg ggcgcattccag gagggccatc ttgcacccct tcactgagag cggcgtatcc	1740
tggcccaggc tgggcttcct cacgcatttc aggagcgcag cccagcgggc catgcaggca	1800
gaggacggga ggctggacgt gttcctgcgc ttccctcccg gcctcttgtc tccgagggtc	1860
aatgccctcc tggccggctc cctgctggcc caaggcgcag accaggccta ccggaccagg	1920
gtggctgagc tcctgcaggg ctgcctgcgc cccgatgcgc cagtctgtgc acggccatc	1980
aacgtgttgc actgcctgca tgagctgcag cacaccgagc tggccgcag cgtggaggag	2040
gccatggaga gcggggccct ggccaggctg accggatcccg cgacccgcgc tgccctggcc	2100
tacccctgc aggtgtccga cgcctgtgcc caggaggcca acctgtccct gagcctcagc	2160
cagggcgtcc ttcaagccct gctccccag ctgcctact gccggaaagct caggctggac	2220
accaaccagt tccaggaccc cgtgatggag ctgctggca gcgtgctgag tggaaaggac	2280
tgtcgcattc agaagatcag cttggcggag aaccagatca gtaacaaagg ggccaaagct	2340
ctggccagat ccctcttggt caacagaagt ctgacccctc tggacccctcg cgtaactcc	2400
attggaccac aaggggccaa ggctggca gacgcttga agatcaaccg caccctgacc	2460
tccctgagcc tccaggccaa caccgttagg gatgatggtg ccaggtccat ggctgaggcc	2520
ttggccctcca accggaccct ctccatgctg cacctgcaga agaacagcat cggcccatg	2580
ggagcccaagc gnatggcaga tgccttgaag cagaacagga gtctgaaaga gctcatgttc	2640
tccagtaata gtatttgta tggaggtgcc aaggccctgg ctgaggccct gaaggtgaac	2700
cagggcctgg agagcctgga cctgcagagc aattccatca gtgacgcagg agtggcagca	2760
ctgatgggggg ccctctgcac caaccagacc ctcctcagcc tcagccctcg agaaaactcc	2820
atcagtcccc agggagccca ggccatcgct catgcctct gcgcacaacag caccctgaag	2880

aacctggacc tgacagccaa cctcctccac gaccagggtg cccgggcat cgcaagtggca 2940  
gtgagagaaa accgcacccct cacctccctt cacctgcagt ggaacttcat ccaggccggc 3000  
gctgcccagg ccctgggaca agcactacag ctcaacagga gcctcaccag ctttagattta 3060  
caggagaacg ccatcgaaaa tgacggagcg tgtgcggtgg cccgtgcact gaaggtcaac 3120  
acagccctca ctgctctcta tctccaggtg gcctcaattt gtgcttcagg cgcccaggtg 3180  
ctaggggaag ccttggctgt gaacagaacc ttggagattc tcgacttaag aggaaatgcc 3240  
attgggggtgg ctggagccaa agccctggca aatgctctga aggtaaactc aagtctccgg 3300  
agactcaatc ttcaagagaa ttctctgggg atggacgggg cgatatgcat tgccacagca 3360  
ctgtctggaa accacaggct ccagcatatc aatctccagg gaaaccacat tggggactcc 3420  
ggggccagga tgatctcaga ggccatcaag acaaattgtc ccacgtgcac tggaaatg 3480  
tgatcctgg 3489

<210> 28  
<211> 1065  
<212> PRT  
<213> Homo sapiens

<400> 28

Met Arg Lys Gln Glu Val Arg Thr Gly Arg Glu Ala Gly Gln Gly His  
1 5 10 15

Gly Thr Gly Ser Pro Ala Glu Gln Val Lys Ala Leu Met Asp Leu Leu  
20 25 30

Ala Gly Lys Gly Ser Gln Gly Ser Gln Ala Pro Gln Ala Leu Asp Arg  
35 40 45

Thr Pro Asp Ala Pro Leu Gly Pro Cys Ser Asn Asp Ser Arg Ile Gln  
50 55 60

Arg His Arg Lys Ala Leu Leu Ser Lys Val Gly Gly Pro Glu Leu  
65 70 75 80

Gly Gly Pro Trp His Arg Leu Ala Ser Leu Leu Leu Val Glu Gly Leu  
85 90 95

Thr Asp Leu Gln Leu Arg Glu His Asp Phe Thr Gln Val Glu Ala Thr  
100 105 110

Arg Gly Gly Gly His Pro Ala Arg Thr Val Ala Leu Asp Arg Leu Phe  
115 120 125

Leu Pro Leu Ser Arg Val Ser Val Pro Pro Arg Val Ser Ile Thr Ile  
130 135 140

Gly Val Ala Gly Met Gly Lys Thr Thr Leu Val Arg His Phe Val Arg  
145 150 155 160

Leu Trp Ala His Gly Gln Val Gly Lys Asp Phe Ser Leu Val Leu Pro  
165 170 175

Leu Thr Phe Arg Asp Leu Asn Thr His Glu Lys Leu Cys Ala Asp Arg  
180 185 190

Leu Ile Cys Ser Val Phe Pro His Val Gly Glu Pro Ser Leu Ala Val  
195 200 205

Ala Val Pro Ala Arg Ala Leu Leu Ile Leu Asp Gly Leu Asp Glu Cys  
210 215 220

Arg Thr Pro Leu Asp Phe Ser Asn Thr Val Ala Cys Thr Asp Pro Lys  
225 230 235 240

Lys Glu Ile Pro Val Asp His Leu Ile Thr Asn Ile Ile Arg Gly Asn  
245 250 255

Leu Phe Pro Glu Val Ser Ile Trp Ile Thr Ser Arg Pro Ser Ala Ser  
260 265 270

Gly Gln Ile Pro Gly Gly Leu Val Asp Arg Met Thr Glu Ile Arg Gly  
275 280 285

Phe Asn Glu Glu Glu Ile Lys Val Cys Leu Glu Gln Met Phe Pro Glu  
290 295 300

Asp Gln Ala Leu Leu Gly Trp Met Leu Ser Gln Val Gln Ala Asp Arg  
305 310 315 320

Ala Leu Tyr Leu Met Cys Thr Val Pro Ala Phe Cys Arg Leu Thr Gly  
325 330 335

Met Ala Leu Gly His Leu Trp Arg Ser Arg Thr Gly Pro Gln Asp Ala  
340 345 350

Glu Leu Trp Pro Pro Arg Thr Leu Cys Glu Leu Tyr Ser Trp Tyr Phe  
355 360 365

Arg Met Ala Leu Ser Gly Glu Gly Gln Glu Lys Gly Lys Ala Ser Pro  
370 375 380

Arg Ile Glu Gln Val Ala His Gly Gly Arg Lys Met Val Gly Thr Leu  
385 390 395 400

Gly Arg Leu Ala Phe His Gly Leu Leu Lys Lys Lys Tyr Val Phe Tyr  
405 410 415

Glu Gln Asp Met Lys Ala Phe Gly Val Asp Leu Ala Leu Leu Gln Gly  
420 425 430

Ala Pro Cys Ser Cys Phe Leu Gln Arg Glu Glu Thr Leu Ala Ser Ser  
435 440 445

Val Ala Tyr Cys Phe Thr His Leu Ser Leu Gln Glu Phe Val Ala Ala  
450 455 460

Ala Tyr Tyr Tyr Gly Ala Ser Arg Arg Ala Ile Phe Asp Leu Phe Thr  
465 470 475 480

Glu Ser Gly Val Ser Trp Pro Arg Leu Gly Phe Leu Thr His Phe Arg  
485 490 495

Ser Ala Ala Gln Arg Ala Met Gln Ala Glu Asp Gly Arg Leu Asp Val  
500 505 510

Phe Leu Arg Phe Leu Ser Gly Leu Leu Ser Pro Arg Val Asn Ala Leu  
515 520 525

Leu Ala Gly Ser Leu Leu Ala Gln Gly Glu His Gln Ala Tyr Arg Thr  
530 535 540

Gln Val Ala Glu Leu Leu Gln Gly Cys Leu Arg Pro Asp Ala Ala Val  
545 550 555 560

Cys Ala Arg Ala Ile Asn Val Leu His Cys Leu His Glu Leu Gln His  
565 570 575

Thr Glu Leu Ala Arg Ser Val Glu Glu Ala Met Glu Ser Gly Ala Leu  
580 585 590

Ala Arg Leu Thr Gly Pro Ala His Arg Ala Ala Leu Ala Tyr Leu Leu  
595 600 605

Gln Val Ser Asp Ala Cys Ala Gln Glu Ala Asn Leu Ser Leu Ser Leu

610

615

620

Ser Gln Gly Val Leu Gln Ser Leu Leu Pro Gln Leu Leu Tyr Cys Arg  
625                   630                   635                   640

Lys Leu Arg Leu Asp Thr Asn Gln Phe Gln Asp Pro Val Met Glu Leu  
645                   650                   655

Leu Gly Ser Val Leu Ser Gly Lys Asp Cys Arg Ile Gln Lys Ile Ser  
660                   665                   670

Leu Ala Glu Asn Gln Ile Ser Asn Lys Gly Ala Lys Ala Leu Ala Arg  
675                   680                   685

Ser Leu Leu Val Asn Arg Ser Leu Thr Ser Leu Asp Leu Arg Gly Asn  
690                   695                   700

Ser Ile Gly Pro Gln Gly Ala Lys Ala Leu Asp Ala Leu Lys Ile  
705                   710                   715                   720

Asn Arg Thr Leu Thr Ser Leu Ser Leu Gln Gly Asn Thr Val Arg Asp  
725                   730                   735

Asp Gly Ala Arg Ser Met Ala Glu Ala Leu Ala Ser Asn Arg Thr Leu  
740                   745                   750

Ser Met Leu His Leu Gln Lys Asn Ser Ile Gly Pro Met Gly Ala Gln  
755                   760                   765

Arg Met Ala Asp Ala Leu Lys Gln Asn Arg Ser Leu Lys Glu Leu Met  
770                   775                   780

Phe Ser Ser Asn Ser Ile Gly Asp Gly Gly Ala Lys Ala Leu Ala Glu  
785                   790                   795                   800

Ala Leu Lys Val Asn Gln Gly Leu Glu Ser Leu Asp Leu Gln Ser Asn  
805                   810                   815

Ser Ile Ser Asp Ala Gly Val Ala Ala Leu Met Gly Ala Leu Cys Thr  
820                   825                   830

Asn Gln Thr Leu Leu Ser Leu Ser Leu Arg Glu Asn Ser Ile Ser Pro  
835                   840                   845

Glu Gly Ala Gln Ala Ile Ala His Ala Leu Cys Ala Asn Ser Thr Leu  
850                   855                   860

Lys Asn Leu Asp Leu Thr Ala Asn Leu Leu His Asp Gln Gly Ala Arg  
865                    870                    875                    880

Ala Ile Ala Val Ala Val Arg Glu Asn Arg Thr Leu Thr Ser Leu His  
885                    890                    895

Leu Gln Trp Asn Phe Ile Gln Ala Gly Ala Ala Gln Ala Leu Gly Gln  
900                    905                    910

Ala Leu Gln Leu Asn Arg Ser Leu Thr Ser Leu Asp Leu Gln Glu Asn  
915                    920                    925

Ala Ile Gly Asp Asp Gly Ala Cys Ala Val Ala Arg Ala Leu Lys Val  
930                    935                    940

Asn Thr Ala Leu Thr Ala Leu Tyr Leu Gln Val Ala Ser Ile Gly Ala  
945                    950                    955                    960

Ser Gly Ala Gln Val Leu Gly Glu Ala Leu Ala Val Asn Arg Thr Leu  
965                    970                    975

Glu Ile Leu Asp Leu Arg Gly Asn Ala Ile Gly Val Ala Gly Ala Lys  
980                    985                    990

Ala Leu Ala Asn Ala Leu Lys Val Asn Ser Ser Leu Arg Arg Leu Asn  
995                    1000                    1005

Leu Gln Glu Asn Ser Leu Gly Met Asp Gly Ala Ile Cys Ile Ala  
1010                    1015                    1020

Thr Ala Leu Ser Gly Asn His Arg Leu Gln His Ile Asn Leu Gln  
1025                    1030                    1035

Gly Asn His Ile Gly Asp Ser Gly Ala Arg Met Ile Ser Glu Ala  
1040                    1045                    1050

Ile Lys Thr Asn Ala Pro Thr Cys Thr Val Glu Met  
1055                    1060                    1065

<210> 29  
<211> 282  
<212> DNA  
<213> Homo sapiens

<400> 29  
atggcaagca cccgctgcaa gctggccagg tacctggagg acctggagga tgtggacttg

aagaaatcta agatgcactt agaggactat cctccccaga agggctgcat ccccccggc 120  
aggggtcaga cagagaaggc agaccatgtg gatctagcca cgctaatgtat cgacttcaat 180  
ggggaggaga aggcgtggc catggccgtg tggatcttcg ctgcgatcaa caggagagac 240  
ctttatgaga aagaaaaag agatgagccg aagtgggtt ag 282

<210> 30  
<211> 93  
<212> PRT  
<213> Homo sapiens

<400> 30

Met Ala Ser Thr Arg Cys Lys Leu Ala Arg Tyr Leu Glu Asp Leu Glu  
1 5 10 15

Asp Val Asp Leu Lys Lys Phe Lys Met His Leu Glu Asp Tyr Pro Pro  
20 25 30

Gln Lys Gly Cys Ile Pro Leu Pro Arg Gly Gln Thr Glu Lys Ala Asp  
35 40 45

His Val Asp Leu Ala Thr Leu Met Ile Asp Phe Asn Gly Glu Glu Lys  
50 55 60

Ala Trp Ala Met Ala Val Trp Ile Phe Ala Ala Ile Asn Arg Arg Asp  
65 70 75 80

Leu Tyr Glu Lys Ala Lys Arg Asp Glu Pro Lys Trp Gly  
85 90

<210> 31  
<211> 2154  
<212> DNA  
<213> Homo sapiens

<400> 31  
atggcaagca cccgctgcaa gctggccagg tacctggagg acctggagga tgtggacttg 60  
aagaaatcta agatgcactt agaggactat cctccccaga agggctgcat ccccccggc 120  
aggggtcaga cagagaaggc agaccatgtg gatctagcca cgctaatgtat cgacttcaat 180  
ggggaggaga aggcgtggc catggccgtg tggatcttcg ctgcgatcaa caggagagac 240  
ctttatgaga aagaaaaag agatgagccg aagtgggtt cagataatgc acgtgtttcg 300  
aatcccactg tgatatgccca ggaagacagc attgaagagg agtggatggg tttactggag 360  
tacctttcga gaatctctat ttgtaaaatg aagaaagatt accgtaagaa gtacagaaag 420

tacgtgagaa	gcagattcca	gtgcattgaa	gacaggaatg	cccgtctggg	tgagagtgtg	480
agcctcaaca	aacgctacac	acgactgcgt	ctcatcaagg	agcacccggag	ccagcaggag	540
agggagcagg	agcttctggc	catcgcaag	accaagacgt	gtgagagccc	cgtgagtccc	600
attaagatgg	agttgctgtt	tgaccccgat	gatgagcatt	ctgagcctgt	gcacaccgtg	660
gtgttccagg	gggcggcagg	gattggaaa	acaatcctgg	ccaggaagat	gatgttggac	720
tgggcgtcgg	ggacactcta	ccaagacagg	tttgactatc	tgttctatat	ccactgtcgg	780
gaggtgagcc	tttgtacaca	gaggagcctg	ggggacctga	tcatgagctg	ctgccccgac	840
ccaaacccac	ccatccacaa	gatcgtgaga	aaaccctcca	gaatccttt	cctcatggac	900
ggcttcgatg	agctgcaagg	tgcctttgac	gagcacatag	gaccgctctg	cactgactgg	960
cagaaggccg	agcggggaga	catttcctg	agcagcctca	tcagaaagaa	gctgcttccc	1020
gaggcctctc	tgctcatcac	cacgagacct	gtggccctgg	agaaactgca	gcacttgctg	1080
gaccatcctc	ggcatgtgga	gatcctgggt	ttctccgagg	ccaaaaggaa	agagtacttc	1140
ttcaagtact	tctctgatga	ggcccaagcc	agggcagcct	tcagtctgat	tcaggagaac	1200
gaggtcctct	tcaccatgtg	tttcatcccc	ctggctctgct	ggatcgtgtg	cactggactg	1260
aaacagcaga	tggagagtgg	caagagcctt	gcccagacat	ccaagaccac	caccgcggtg	1320
tacgtttct	tcctttccag	tttgcgcag	ccccggggag	ggagccagga	gcacggcctc	1380
tgcgccacc	tctgggggct	ctgcttttg	gctgcagatg	gaatctggaa	ccagaaaatc	1440
ctgtttgagg	agtccgacct	caggaatcat	ggactgcaga	aggcggatgt	gtctgcttc	1500
ctgaggatga	acctgttcca	aaaggaagtg	gactgcgaga	agttctacag	tttcatccac	1560
atgactttcc	aggagttctt	tgccgccatg	tactacctgc	tggaagagga	aaaggaagga	1620
aggacgaacg	ttccagggag	tcgttgaag	cttcccagcc	gagacgtgac	agtccttctg	1680
gaaaactatg	gcaaattcga	aaagggat	ttgattttg	ttgtacgtt	cctctttggc	1740
ctggtaaacc	aggagaggac	ctcctacttg	gagaagaaat	taagttgcaa	gatctctcag	1800
caaatcaggc	tggagctgct	gaaatggatt	gaagtgaaag	ccaaagctaa	aaagctgcag	1860
atccagccca	gccagctgga	attgttctac	tgtttgtacg	agatgcagga	ggaggacttc	1920
gtgcaaagg	ccatggacta	tttccccaaag	attgagatca	atctctccac	cagaatggac	1980
cacatggttt	tttccttttg	cattgagaac	tgtcatcggg	tggagtcact	gtccctgggg	2040
tttctccata	acatgccccaa	ggaggaagag	gaggagaaaa	aggaaggccg	acaccttgc	2100
atggtgcagt	gtgtcctccc	aagctcctct	catgctgcct	gttctcatgg	atag	2154

<210> 32  
<211> 717

<212> PRT

<213> Homo sapiens

<400> 32

Met Ala Ser Thr Arg Cys Lys Leu Ala Arg Tyr Leu Glu Asp Leu Glu  
1 5 10 15

Asp Val Asp Leu Lys Lys Phe Lys Met His Leu Glu Asp Tyr Pro Pro  
20 25 30

Gln Lys Gly Cys Ile Pro Leu Pro Arg Gly Gln Thr Glu Lys Ala Asp  
35 40 45

His Val Asp Leu Ala Thr Leu Met Ile Asp Phe Asn Gly Glu Glu Lys  
50 55 60

Ala Trp Ala Met Ala Val Trp Ile Phe Ala Ala Ile Asn Arg Arg Asp  
65 70 75 80

Leu Tyr Glu Lys Ala Lys Arg Asp Glu Pro Lys Trp Gly Ser Asp Asn  
85 90 95

Ala Arg Val Ser Asn Pro Thr Val Ile Cys Gln Glu Asp Ser Ile Glu  
100 105 110

Glu Glu Trp Met Gly Leu Leu Glu Tyr Leu Ser Arg Ile Ser Ile Cys  
115 120 125

Lys Met Lys Lys Asp Tyr Arg Lys Lys Tyr Arg Lys Tyr Val Arg Ser  
130 135 140

Arg Phe Gln Cys Ile Glu Asp Arg Asn Ala Arg Leu Gly Glu Ser Val  
145 150 155 160

Ser Leu Asn Lys Arg Tyr Thr Arg Leu Arg Leu Ile Lys Glu His Arg  
165 170 175

Ser Gln Gln Glu Arg Glu Gln Glu Leu Leu Ala Ile Gly Lys Thr Lys  
180 185 190

Thr Cys Glu Ser Pro Val Ser Pro Ile Lys Met Glu Leu Leu Phe Asp  
195 200 205

Pro Asp Asp Glu His Ser Glu Pro Val His Thr Val Val Phe Gln Gly  
210 215 220

Ala Ala Gly Ile Gly Lys Thr Ile Leu Ala Arg Lys Met Met Leu Asp  
225 230 235 240

Trp Ala Ser Gly Thr Leu Tyr Gln Asp Arg Phe Asp Tyr Leu Phe Tyr  
245 250 255

Ile His Cys Arg Glu Val Ser Leu Val Thr Gln Arg Ser Leu Gly Asp  
260 265 270

Leu Ile Met Ser Cys Cys Pro Asp Pro Asn Pro Pro Ile His Lys Ile  
275 280 285

Val Arg Lys Pro Ser Arg Ile Leu Phe Leu Met Asp Gly Phe Asp Glu  
290 295 300

Leu Gln Gly Ala Phe Asp Glu His Ile Gly Pro Leu Cys Thr Asp Trp  
305 310 315 320

Gln Lys Ala Glu Arg Gly Asp Ile Leu Leu Ser Ser Leu Ile Arg Lys  
325 330 335

Lys Leu Leu Pro Glu Ala Ser Leu Leu Ile Thr Thr Arg Pro Val Ala  
340 345 350

Leu Glu Lys Leu Gln His Leu Leu Asp His Pro Arg His Val Glu Ile  
355 360 365

Leu Gly Phe Ser Glu Ala Lys Arg Lys Glu Tyr Phe Phe Lys Tyr Phe  
370 375 380

Ser Asp Glu Ala Gln Ala Arg Ala Ala Phe Ser Leu Ile Gln Glu Asn  
385 390 395 400

Glu Val Leu Phe Thr Met Cys Phe Ile Pro Leu Val Cys Trp Ile Val  
405 410 415

Cys Thr Gly Leu Lys Gln Gln Met Glu Ser Gly Lys Ser Leu Ala Gln  
420 425 430

Thr Ser Lys Thr Thr Ala Val Tyr Val Phe Phe Leu Ser Ser Leu  
435 440 445

Leu Gln Pro Arg Gly Ser Gln Glu His Gly Leu Cys Ala His Leu  
450 455 460

Trp Gly Leu Cys Ser Leu Ala Ala Asp Gly Ile Trp Asn Gln Lys Ile

465

470

475

480

Leu Phe Glu Glu Ser Asp Leu Arg Asn His Gly Leu Gln Lys Ala Asp  
485 490 495

Val Ser Ala Phe Leu Arg Met Asn Leu Phe Gln Lys Glu Val Asp Cys  
500 505 510

Glu Lys Phe Tyr Ser Phe Ile His Met Thr Phe Gln Glu Phe Phe Ala  
515 520 525

Ala Met Tyr Tyr Leu Leu Glu Glu Lys Glu Gly Arg Thr Asn Val  
530 535 540

Pro Gly Ser Arg Leu Lys Leu Pro Ser Arg Asp Val Thr Val Leu Leu  
545 550 555 560

Glu Asn Tyr Gly Lys Phe Glu Lys Gly Tyr Leu Ile Phe Val Val Arg  
565 570 575

Phe Leu Phe Gly Leu Val Asn Gln Glu Arg Thr Ser Tyr Leu Glu Lys  
580 585 590

Lys Leu Ser Cys Lys Ile Ser Gln Gln Ile Arg Leu Glu Leu Leu Lys  
595 600 605

Trp Ile Glu Val Lys Ala Lys Ala Lys Lys Leu Gln Ile Gln Pro Ser  
610 615 620

Gln Leu Glu Leu Phe Tyr Cys Leu Tyr Glu Met Gln Glu Glu Asp Phe  
625 630 635 640

Val Gln Arg Ala Met Asp Tyr Phe Pro Lys Ile Glu Ile Asn Leu Ser  
645 650 655

Thr Arg Met Asp His Met Val Ser Ser Phe Cys Ile Glu Asn Cys His  
660 665 670

Arg Val Glu Ser Leu Ser Leu Gly Phe Leu His Asn Met Pro Lys Glu  
675 680 685

Glu Glu Glu Glu Lys Glu Gly Arg His Leu Asp Met Val Gln Cys  
690 695 700

Val Leu Pro Ser Ser His Ala Ala Cys Ser His Gly  
705 710 715

<210> 33  
 <211> 2835  
 <212> DNA  
 <213> Homo sapiens

<400> 33  
 atggcaagca cccgctgcaa gctggccagg taccccactg tgatatgccaa ggaagacagc 60  
 attgaagagg agtggatggg tttactggag taccttcga gaatctctat ttgtaaaatg 120  
 aagaaaagatt accgtaagaa gtacagaaag tacgtgagaa gcagattcca gtgcattgaa 180  
 gacaggaatg cccgtctggg tgagagtgtg agcctcaaca aacgctacac acgactgcgt 240  
 ctcatcaagg agcaccggag ccagcaggag agggagcagg agcttctggc catcgcaag 300  
 accaagacgt gtgagagccc cgtgagtccc attaagatgg agttgctgtt tgaccccgat 360  
 gatgagcatt ctgagcctgt gcacaccgtg gtgttccagg gggcggcagg gattggaaa 420  
 acaatcctgg ccaggaagat gatgttggac tgggcgtcgg ggacactcta ccaagacagg 480  
 tttgactatac tttctatat ccactgtcgg gaggtgagcc ttgtgacaca gaggagcctg 540  
 ggggacctga tcatgagctg ctgccccac ccaaaccac ccatccacaa gatcgtgaga 600  
 aaaccctcca gaatcctctt cctcatggac ggcttcgatg agctgcaagg tgcctttgac 660  
 gagcacatag gaccgctctg cactgactgg cagaaggccg agcggggaga cattctcctg 720  
 agcagcctca tcagaaagaa gctgcttccc gaggcctctc tgctcatcac cacgagacct 780  
 gtggccctgg agaaaactgca gcacttgctg gaccatcctc ggcattgtgg gatcctgggt 840  
 ttctccgagg ccaaaaggaa agagtaatcc ttcaagtact tctctgtatgaa ggcccaagcc 900  
 agggcagcct tcagtctgat tcaggagaac gaggtcctct tcaccatgtg cttcatcccc 960  
 ctggtctgct ggatcgtgtg cactggactg aaacagcaga tggagagtgg caagagcctt 1020  
 gcccagacat ccaagaccac caccgcggtg tacgtcttct tcctttccag tttgctgcag 1080  
 ccccggggag ggagccagga gcacggcctc tgcccccacc tctggggct ctgctcttg 1140  
 gctgcagatg gaatctggaa ccagaaaatc ctgtttgagg agtccgaccc caggaatcat 1200  
 ggactgcaga aggccggatgt gtctgcttcc ctgaggatga acctgttcca aaaggaagtg 1260  
 gactgcgaga agttctacag cttcatccac atgactttcc aggagttctt tgccgcccattg 1320  
 tactacctgc tggaaagagga aaaggaagga aggacgaacg ttccaggag tggatgg 1380  
 cttcccagcc gagacgtgac agtccttctg gaaaactatg gcaaattcga aaaggggtat 1440  
 ttgattttg ttgtacgttt cctcttggc ctggtaaacc aggagaggac ctcctacttg 1500  
 gagaagaaat taagttgcaa gatctctcag caaatcaggc tggagctgct gaaatggatt 1560  
 gaagtgaaag ccaaaagctaa aaagctgcag atccagccca gccagctgga attgttctac 1620

tgttgtacg agatgcagga ggaggacttc gtgcaaaggg ccatggacta tttcccaag	1680
attgagatca atctctccac cagaatggac cacatggttt cttccctttg cattgagaac	1740
tgtcatcggg tggagtcact gtccctgggg tttctccata acatgccc aa ggaggaagag	1800
gaggagggaaa aggaaggccg acaccctgat atggtgcagt gtgcctccc aagctccct	1860
catgctgcct gttctcatgg attggtaac agccaccta cttccagttt ttgccgggc	1920
ctctttcag ttctgagcac cagccagagt ctaactaat tggacctcag tgacaattct	1980
ctgggggacc cagggatgag agtgggtgt gaaacgctcc agcatcctgg ctgtaacatt	2040
cggagattgt gggtggggcg ctgtggcctc tcgcatgagt gctgcttcga catctccttg	2100
gtcctcagca gcaaccagaa gctggtgag ctggacctga gtgacaacgc ctcggtgac	2160
ttcggaatca gacttctgtg tgtggactg aagcacctgt tgtcaatct gaagaagctc	2220
tggttggtca gctgctgcct cacatcagca tgggtcagg atctgcattc agtattgagc	2280
accagccatt ccctgaccag actctatgtg ggggagaatg cttggaga ctcaggagtc	2340
gcaattttat gtaaaaaagc caagaatcca cagtgttaacc tgcagaaact ggggttggtg	2400
aattctggcc ttacgtcagt ctgtgttca gctttgtcct cggtactcag cactaatcag	2460
aatctcacgc acctttaccc gcgaggcaac actctcgag acaagggat caaactactc	2520
tgtgaggac tcttgcaccc cgactgcaag cttcaggtgt tggattttaga caactgcaac	2580
ctcacgtcac actgctgctg ggatcttcc acacttctga cttccagcca gagcctgcga	2640
aagctgagcc tggcaacaa tgacctggc gacctgggg tcatgatgtt ctgtgaagt	2700
ctgaaacagc agagctgcct ctcagaac ctgggttgt ctgaaatgtt tttcaattat	2760
gagacaaaaa gtgcgttaga aacacttcaa gaagaaaagc ctgagctgac cgtcgcttt	2820
gagccttctt ggtag	2835

<210> 34  
 <211> 944  
 <212> PRT  
 <213> Homo sapiens

<400> 34

Met	Ala	Ser	Thr	Arg	Cys	Lys	Leu	Ala	Arg	Tyr	Pro	Thr	Val	Ile	Cys
1							5		10					15	

Gln	Glu	Asp	Ser	Ile	Glu	Glu	Trp	Met	Gly	Leu	Leu	Glu	Tyr	Leu
				20				25				30		

Ser	Arg	Ile	Ser	Ile	Cys	Lys	Met	Lys	Lys	Asp	Tyr	Arg	Lys	Lys	Tyr
					35			40				45			

Arg Lys Tyr Val Arg Ser Arg Phe Gln Cys Ile Glu Asp Arg Asn Ala  
50 55 60

Arg Leu Gly Glu Ser Val Ser Leu Asn Lys Arg Tyr Thr Arg Leu Arg  
65 70 75 80

Leu Ile Lys Glu His Arg Ser Gln Gln Glu Arg Glu Gln Glu Leu Leu  
85 90 95

Ala Ile Gly Lys Thr Lys Thr Cys Glu Ser Pro Val Ser Pro Ile Lys  
100 105 110

Met Glu Leu Leu Phe Asp Pro Asp Asp Glu His Ser Glu Pro Val His  
115 120 125

Thr Val Val Phe Gln Gly Ala Ala Gly Ile Gly Lys Thr Ile Leu Ala  
130 135 140

Arg Lys Met Met Leu Asp Trp Ala Ser Gly Thr Leu Tyr Gln Asp Arg  
145 150 155 160

Phe Asp Tyr Leu Phe Tyr Ile His Cys Arg Glu Val Ser Leu Val Thr  
165 170 175

Gln Arg Ser Leu Gly Asp Leu Ile Met Ser Cys Cys Pro Asp Pro Asn  
180 185 190

Pro Pro Ile His Lys Ile Val Arg Lys Pro Ser Arg Ile Leu Phe Leu  
195 200 205

Met Asp Gly Phe Asp Glu Leu Gln Gly Ala Phe Asp Glu His Ile Gly  
210 215 220

Pro Leu Cys Thr Asp Trp Gln Lys Ala Glu Arg Gly Asp Ile Leu Leu  
225 230 235 240

Ser Ser Leu Ile Arg Lys Lys Leu Leu Pro Glu Ala Ser Leu Leu Ile  
245 250 255

Thr Thr Arg Pro Val Ala Leu Glu Lys Leu Gln His Leu Leu Asp His  
260 265 270

Pro Arg His Val Glu Ile Leu Gly Phe Ser Glu Ala Lys Arg Lys Glu  
275 280 285

Tyr Phe Phe Lys Tyr Phe Ser Asp Glu Ala Gln Ala Arg Ala Ala Phe  
290 295 300

Ser Leu Ile Gln Glu Asn Glu Val Leu Phe Thr Met Cys Phe Ile Pro  
305 310 315 320

Leu Val Cys Trp Ile Val Cys Thr Gly Leu Lys Gln Gln Met Glu Ser  
325 330 335

Gly Lys Ser Leu Ala Gln Thr Ser Lys Thr Thr Thr Ala Val Tyr Val  
340 345 350

Phe Phe Leu Ser Ser Leu Leu Gln Pro Arg Gly Gly Ser Gln Glu His  
355 360 365

Gly Leu Cys Ala His Leu Trp Gly Leu Cys Ser Leu Ala Ala Asp Gly  
370 375 380

Ile Trp Asn Gln Lys Ile Leu Phe Glu Glu Ser Asp Leu Arg Asn His  
385 390 395 400

Gly Leu Gln Lys Ala Asp Val Ser Ala Phe Leu Arg Met Asn Leu Phe  
405 410 415

Gln Lys Glu Val Asp Cys Glu Lys Phe Tyr Ser Phe Ile His Met Thr  
420 425 430

Phe Gln Glu Phe Phe Ala Ala Met Tyr Tyr Leu Leu Glu Glu Glu Lys  
435 440 445

Glu Gly Arg Thr Asn Val Pro Gly Ser Arg Leu Lys Leu Pro Ser Arg  
450 455 460

Asp Val Thr Val Leu Leu Glu Asn Tyr Gly Lys Phe Glu Lys Gly Tyr  
465 470 475 480

Leu Ile Phe Val Val Arg Phe Leu Phe Gly Leu Val Asn Gln Glu Arg  
485 490 495

Thr Ser Tyr Leu Glu Lys Lys Leu Ser Cys Lys Ile Ser Gln Gln Ile  
500 505 510

Arg Leu Glu Leu Leu Lys Trp Ile Glu Val Lys Ala Lys Ala Lys Lys  
515 520 525

Leu Gln Ile Gln Pro Ser Gln Leu Glu Leu Phe Tyr Cys Leu Tyr Glu  
530 535 540

Met Gln Glu Glu Asp Phe Val Gln Arg Ala Met Asp Tyr Phe Pro Lys  
545 550 555 560

Ile Glu Ile Asn Leu Ser Thr Arg Met Asp His Met Val Ser Ser Phe  
565 570 575

Cys Ile Glu Asn Cys His Arg Val Glu Ser Leu Ser Leu Gly Phe Leu  
580 585 590

His Asn Met Pro Lys Glu Glu Glu Glu Lys Glu Gly Arg His  
595 600 605

Leu Asp Met Val Gln Cys Val Leu Pro Ser Ser His Ala Ala Cys  
610 615 620

Ser His Gly Leu Val Asn Ser His Leu Thr Ser Ser Phe Cys Arg Gly  
625 630 635 640

Leu Phe Ser Val Leu Ser Thr Ser Gln Ser Leu Thr Glu Leu Asp Leu  
645 650 655

Ser Asp Asn Ser Leu Gly Asp Pro Gly Met Arg Val Leu Cys Glu Thr  
660 665 670

Leu Gln His Pro Gly Cys Asn Ile Arg Arg Leu Trp Leu Gly Arg Cys  
675 680 685

Gly Leu Ser His Glu Cys Cys Phe Asp Ile Ser Leu Val Leu Ser Ser  
690 695 700

Asn Gln Lys Leu Val Glu Leu Asp Leu Ser Asp Asn Ala Leu Gly Asp  
705 710 715 720

Phe Gly Ile Arg Leu Leu Cys Val Gly Leu Lys His Leu Leu Cys Asn  
725 730 735

Leu Lys Lys Leu Trp Leu Val Ser Cys Cys Leu Thr Ser Ala Cys Cys  
740 745 750

Gln Asp Leu Ala Ser Val Leu Ser Thr Ser His Ser Leu Thr Arg Leu  
755 760 765

Tyr Val Gly Glu Asn Ala Leu Gly Asp Ser Gly Val Ala Ile Leu Cys

770

775

780

Glu Lys Ala Lys Asn Pro Gln Cys Asn Leu Gln Lys Leu Gly Leu Val  
 785                    790                    795                    800

Asn Ser Gly Leu Thr Ser Val Cys Cys Ser Ala Leu Ser Ser Val Leu  
 805                    810                    815

Ser Thr Asn Gln Asn Leu Thr His Leu Tyr Leu Arg Gly Asn Thr Leu  
 820                    825                    830

Gly Asp Lys Gly Ile Lys Leu Leu Cys Glu Gly Leu Leu His Pro Asp  
 835                    840                    845

Cys Lys Leu Gln Val Leu Glu Leu Asp Asn Cys Asn Leu Thr Ser His  
 850                    855                    860

Cys Cys Trp Asp Leu Ser Thr Leu Leu Thr Ser Ser Gln Ser Leu Arg  
 865                    870                    875                    880

Lys Leu Ser Leu Gly Asn Asn Asp Leu Gly Asp Leu Gly Val Met Met  
 885                    890                    895

Phe Cys Glu Val Leu Lys Gln Gln Ser Cys Leu Leu Gln Asn Leu Gly  
 900                    905                    910

Leu Ser Glu Met Tyr Phe Asn Tyr Glu Thr Lys Ser Ala Leu Glu Thr  
 915                    920                    925

Leu Gln Glu Glu Lys Pro Glu Leu Thr Val Val Phe Glu Pro Ser Trp  
 930                    935                    940

<210> 35  
<211> 993  
<212> DNA  
<213> Homo sapiens

<400> 35		
atggcaagca cccgctgcaa gctggccagg taccatggat tggtaaacag ccacacct		60
tccagttttt gccggggcct ctttcagtt ctgagcacca gccagagtct aactgaattt		120
gacctcagtg acaattctct gggggaccca gggatgagag tgggtgtga aacgctccag		180
catcctggct gtaacattcg gagattgtgg ttggggcgct gtggcctctc gcatgagtgc		240
tgcttcgaca tctccttggt cctcagcagc aaccagaagc tggtggagct ggacctgagt		300
gacaacgccc tcggtgactt cggaatcaga cttctgtgtg tgggactgaa gcacctgttg		360

tgcaatctga	agaagctctg	gttggtcagc	tgctgcctca	catcagcatg	ttgtcaggat	420
cttgcacatcg	tattgagcac	cagccattcc	ctgaccagac	tctatgtggg	ggagaatgcc	480
ttgggagact	caggagtcgc	aatttatgt	aaaaaagcca	agaatccaca	gtgtAACCTG	540
cagaaactgg	ggttggtaaa	ttctggcctt	acgtcagtct	gttgttcagc	tttgtcctcg	600
gtactcagca	ctaattcagaa	tctcacgcac	cttacactgc	gaggcaacac	tctcgagac	660
aaggggatca	aactactctg	tgagggactc	ttgcaccccg	actgcaagct	tcaggtgttg	720
gaatttagaca	actgcaacct	cacgtcacac	tgctgctggg	atcttccac	acttctgacc	780
tccagccaga	gcctgcgaaa	gctgagcctg	ggcaacaatg	acctggcgaa	cctgggggtc	840
atgatgttct	gtgaagtgt	gaaacagcag	agctgcctcc	tgcagaacct	ggggttgtct	900
gaaatgtatt	tcaattatga	gacaaaaagt	gcgttagaaa	cacttcaaga	agaaaagcct	960
gagctgaccg	tcgtcttga	gccttcttgg	tag			993

<210> 36  
 <211> 330  
 <212> PRT  
 <213> Homo sapiens

<400> 36

Met	Ala	Ser	Thr	Arg	Cys	Lys	Leu	Ala	Arg	Tyr	His	Gly	Leu	Val	Asn
1															15

Ser	His	Leu	Thr	Ser	Ser	Phe	Cys	Arg	Gly	Leu	Phe	Ser	Val	Leu	Ser
															30
20															

Thr	Ser	Gln	Ser	Leu	Thr	Glu	Leu	Asp	Leu	Ser	Asp	Asn	Ser	Leu	Gly
35															45

Asp	Pro	Gly	Met	Arg	Val	Leu	Cys	Glu	Thr	Leu	Gln	His	Pro	Gly	Cys
50															60

Asn	Ile	Arg	Arg	Leu	Trp	Leu	Gly	Arg	Cys	Gly	Leu	Ser	His	Glu	Cys
65															80

Cys	Phe	Asp	Ile	Ser	Leu	Val	Leu	Ser	Ser	Asn	Gln	Lys	Leu	Val	Glu
85															95

Leu	Asp	Leu	Ser	Asp	Asn	Ala	Leu	Gly	Asp	Phe	Gly	Ile	Arg	Leu	Leu
100															110

Cys	Val	Gly	Leu	Lys	His	Leu	Leu	Cys	Asn	Leu	Lys	Lys	Leu	Trp	Leu
115															125

Val Ser Cys Cys Leu Thr Ser Ala Cys Cys Gln Asp Leu Ala Ser Val  
130 135 140

Leu Ser Thr Ser His Ser Leu Thr Arg Leu Tyr Val Gly Glu Asn Ala  
145 150 155 160

Leu Gly Asp Ser Gly Val Ala Ile Leu Cys Glu Lys Ala Lys Asn Pro  
165 170 175

Gln Cys Asn Leu Gln Lys Leu Gly Leu Val Asn Ser Gly Leu Thr Ser  
180 185 190

Val Cys Cys Ser Ala Leu Ser Ser Val Leu Ser Thr Asn Gln Asn Leu  
195 200 205

Thr His Leu Tyr Leu Arg Gly Asn Thr Leu Gly Asp Lys Gly Ile Lys  
210 215 220

Leu Leu Cys Glu Gly Leu Leu His Pro Asp Cys Lys Leu Gln Val Leu  
225 230 235 240

Glu Leu Asp Asn Cys Asn Leu Thr Ser His Cys Cys Trp Asp Leu Ser  
245 250 255

Thr Leu Leu Thr Ser Ser Gln Ser Leu Arg Lys Leu Ser Leu Gly Asn  
260 265 270

Asn Asp Leu Gly Asp Leu Gly Val Met Met Phe Cys Glu Val Leu Lys  
275 280 285

Gln Gln Ser Cys Leu Leu Gln Asn Leu Gly Leu Ser Glu Met Tyr Phe  
290 295 300

Asn Tyr Glu Thr Lys Ser Ala Leu Glu Thr Leu Gln Glu Lys Pro  
305 310 315 320

Glu Leu Thr Val Val Phe Glu Pro Ser Trp  
325 330

<210> 37

<211> 8

<212> PRT

<213> Homo sapiens

<400> 37

Gly Ala Ala Gly Ile Gly Lys Thr

1

5

<210> 38  
<211> 8  
<212> PRT  
<213> Homo sapiens

<400> 38

Gly Asp Ala Gly Val Gly Lys Ser  
1 5

<210> 39  
<211> 8  
<212> PRT  
<213> Homo sapiens

<400> 39

Gly Ser Ala Gly Thr Gly Lys Thr  
1 5

<210> 40  
<211> 8  
<212> PRT  
<213> Homo sapiens

<400> 40

Gly Ala Ala Gly Val Gly Lys Thr  
1 5

<210> 41  
<211> 8  
<212> PRT  
<213> Homo sapiens

<400> 41

Gly Pro Ala Gly Thr Gly Lys Thr  
1 5

<210> 42  
<211> 8  
<212> PRT  
<213> Homo sapiens

<400> 42

Gly Thr Val Gly Thr Gly Lys Ser  
1 5

<210> 43  
<211> 8  
<212> PRT

<213> Homo sapiens

<400> 43

Gly Lys Ala Gly Gln Gly Lys Ser  
1 5

<210> 44

<211> 8

<212> PRT

<213> Homo sapiens

<400> 44

Gly Glu Ala Gly Ser Gly Lys Ser  
1 5

<210> 45

<211> 8

<212> PRT

<213> Homo sapiens

<400> 45

Gly Lys Ala Gly Met Gly Lys Thr  
1 5

<210> 46

<211> 8

<212> PRT

<213> Homo sapiens

<400> 46

Gly Val Ala Gly Met Gly Lys Thr  
1 5

<210> 47

<211> 8

<212> PRT

<213> Homo sapiens

<400> 47

Gly Ala Ala Gly Ile Gly Lys Ser  
1 5

<210> 48

<211> 8

<212> PRT

<213> Homo sapiens

<400> 48

Gly Pro Ala Gly Leu Gly Lys Thr  
1 5

<210> 49  
<211> 8  
<212> PRT  
<213> Homo sapiens

<400> 49

Gly Pro Asp Gly Ile Gly Lys Thr  
1 5

<210> 50  
<211> 8  
<212> PRT  
<213> Homo sapiens

<400> 50

Gly Ala Pro Gly Ile Gly Lys Thr  
1 5

<210> 51  
<211> 8  
<212> PRT  
<213> Homo sapiens

<400> 51

Gly Ala Ala Gly Ile Gly Lys Ser  
1 5

<210> 52  
<211> 8  
<212> PRT  
<213> Homo sapiens

<400> 52

Gly Pro Ala Gly Val Gly Lys Thr  
1 5

<210> 53  
<211> 8  
<212> PRT  
<213> Homo sapiens

<400> 53

Gly Pro Gln Gly Ile Gly Lys Thr  
1 5

<210> 54  
<211> 8  
<212> PRT  
<213> Homo sapiens

<400> 54

Gly Glu Arg Ala Ser Gly Lys Thr  
1 5

<210> 55

<211> 8

<212> PRT

<213> Homo sapiens

<400> 55

Gly Arg Ala Gly Val Gly Lys Thr  
1 5

<210> 56

<211> 8

<212> PRT

<213> Homo sapiens

<400> 56

Gly Lys Ser Gly Ile Gly Lys Ser  
1 5

<210> 57

<211> 8

<212> PRT

<213> Homo sapiens

<400> 57

Ala Cys Ala Gly Thr Gly Lys Thr  
1 5

<210> 58

<211> 8

<212> PRT

<213> Homo sapiens

<400> 58

Gly Met Ala Gly Cys Gly Lys Ser  
1 5

<210> 59

<211> 8

<212> PRT

<213> Homo sapiens

<400> 59

Gly Met Gly Gly Ser Gly Lys Thr  
1 5

<210> 60  
<211> 8  
<212> PRT  
<213> Homo sapiens  
  
<400> 60  
  
Gly Glu Ala Gly Ser Gly Lys Thr  
1 5

<210> 61  
<211> 8  
<212> PRT  
<213> Homo sapiens  
  
<400> 61  
  
Gly Asp Pro Gly Lys Gly Lys Thr  
1 5

<210> 62  
<211> 8  
<212> PRT  
<213> Homo sapiens  
  
<400> 62  
  
Gly Gln Ser Gly Gln Gly Lys Thr  
1 5

<210> 63  
<211> 8  
<212> PRT  
<213> Homo sapiens  
  
<400> 63

Gly Ala Gly Glu Ser Gly Lys Ser  
1 5

<210> 64  
<211> 4  
<212> PRT  
<213> Homo sapiens  
  
<400> 64

Asp Ala Tyr Gly  
1

<210> 65  
<211> 4  
<212> PRT  
<213> Homo sapiens

<400> 65

Asp Glu Pro Gly  
1

<210> 66  
<211> 4  
<212> PRT  
<213> Homo sapiens

<400> 66

Asp Glu Leu Gly  
1

<210> 67  
<211> 4  
<212> PRT  
<213> Homo sapiens

<400> 67

Asp Ile Cys Gly  
1

<210> 68  
<211> 4  
<212> PRT  
<213> Homo sapiens

<400> 68

Asp Asp Leu Gly  
1

<210> 69  
<211> 4  
<212> PRT  
<213> Homo sapiens

<400> 69

Asp Pro Val Gly  
1

<210> 70  
<211> 4  
<212> PRT  
<213> Homo sapiens

<400> 70

Asp Lys Ser Gly  
1

<210> 71  
<211> 4  
<212> PRT  
<213> Homo sapiens

<400> 71

Asp His Ala Gly  
1

<210> 72  
<211> 4  
<212> PRT  
<213> Homo sapiens

<400> 72

Asp Gln Asn Gly  
1

<210> 73  
<211> 4  
<212> PRT  
<213> Homo sapiens

<400> 73

Asp Lys Leu Gly  
1

<210> 74  
<211> 5  
<212> PRT  
<213> Homo sapiens

<400> 74

Leu Phe Leu Met Asp  
1 5

<210> 75  
<211> 5  
<212> PRT  
<213> Homo sapiens

<400> 75

Leu Phe Thr Phe Asp  
1 5

<210> 76  
<211> 5  
<212> PRT  
<213> Homo sapiens

<400> 76

Leu Phe Ile Leu Asp  
1 5

<210> 77  
<211> 5  
<212> PRT  
<213> Homo sapiens

<400> 77

Leu Phe Ile Ile Asp  
1 5

<210> 78  
<211> 5  
<212> PRT  
<213> Homo sapiens

<400> 78

Leu Phe Ile Met Asp  
1 5

<210> 79  
<211> 5  
<212> PRT  
<213> Homo sapiens

<400> 79

Leu Leu Ile Leu Asp  
1 5

<210> 80  
<211> 5  
<212> PRT  
<213> Homo sapiens

<400> 80

Leu Leu Thr Phe Asp  
1 5

<210> 81  
<211> 5  
<212> PRT  
<213> Homo sapiens

<400> 81

Leu Leu Ile Phe Asp  
1 5

<210> 82

<211> 5  
<212> PRT  
<213> Homo sapiens

<400> 82

Leu Phe Val Ile Asp  
1 5

<210> 83  
<211> 5  
<212> PRT  
<213> Homo sapiens

<400> 83

Leu Leu Leu Leu Asp  
1 5

<210> 84  
<211> 6  
<212> PRT  
<213> Homo sapiens

<400> 84

Leu Phe Ile Leu Glu Asp  
1 5

<210> 85  
<211> 5  
<212> PRT  
<213> Homo sapiens

<400> 85

Ile Val Val Leu Asp  
1 5

<210> 86  
<211> 5  
<212> PRT  
<213> Homo sapiens

<400> 86

Leu Phe Leu Leu Asp  
1 5

<210> 87  
<211> 5  
<212> PRT  
<213> Homo sapiens

<400> 87

Tyr Leu Ile Ile Asp  
1 5

<210> 88  
<211> 5  
<212> PRT  
<213> Homo sapiens

<400> 88

Val Leu Ile Ile Asp  
1 5

<210> 89  
<211> 4  
<212> PRT  
<213> Homo sapiens

<400> 89

Ser Lys Ala Asp  
1

<210> 90  
<211> 4  
<212> PRT  
<213> Homo sapiens

<400> 90

Thr Lys His Asp  
1

<210> 91  
<211> 4  
<212> PRT  
<213> Homo sapiens

<400> 91

Ser Lys Gln Asp  
1

<210> 92  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Consensus P-Loop Motif

<220>  
<221> MISC\_FEATURE  
<222> (2)..(5)  
<223> "Xaa" denotes any amino acid residue

<220>  
<221> MISC\_FEATURE  
<222> (8)..(8)  
<223> "Xaa" denotes Serine or Threonine.

<400> 92

Gly Xaa Xaa Xaa Xaa Gly Lys Xaa  
1 5

<210> 93  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Consensus Mg+2 Site (G3)

<220>  
<221> MISC\_FEATURE  
<222> (2)..(4)  
<223> "Xaa" denotes any amino acid residue

<400> 93

Asp Xaa Xaa Gly  
1

<210> 94  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Consensus Mg+2 Site (Kinase2)

<220>  
<221> MISC\_FEATURE  
<222> (1)..(4)  
<223> "Xaa" denotes a hydrophobic amino acid residue

<400> 94

Xaa Xaa Xaa Xaa Asp  
1 5

<210> 95  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Consensus Guanine-binding site (G3)

```

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> "Xaa" denotes Asn, Ser, or Thr

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> "Xaa" denotes any amino acid residue

<400> 95

Xaa Lys Xaa Asp
1

<210> 96
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic primer

<400> 96
tgctacaagt ccgggacaaa                                20

<210> 97
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic primer

<400> 97
gcccagttct gggtcattt                                19

<210> 98
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic probe

<400> 98
cagcagagcc tcagagtgct tcg                                23

<210> 99
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic primer

<400> 99

```

gctgctggca ccagactt

18

<210> 100  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic primer

<400> 100  
cggttaccac atccaagg

18

<210> 101  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic probe

<400> 101  
caaattaccc actccccgacc cg

22

<210> 102  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic primer

<400> 102  
agaccctgcc gcgctact

18

<210> 103  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic primer

<400> 103  
tccactggag ggtgtgagaa c

21

<210> 104  
<211> 15  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic probe

<400> 104  
aaccagagcg aggcc

15

<210> 105	
<211> 19	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic primer	
<400> 105	
gggaccggga gacacagat	19
<210> 106	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic primer	
<400> 106	
gcgcagggttc tctcggtaaag	20
<210> 107	
<211> 16	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic probe	
<400> 107	
caagaccaac acacag	16
<210> 108	
<211> 19	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic primer	
<400> 108	
gccgcaggc tattgctta	19
<210> 109	
<211> 22	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic primer	
<400> 109	
catattgaca acgcctccag aa	22

<210> 110  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic probe

<400> 110  
cactcacaga gacagct

17

<210> 111  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic primer

<400> 111  
acctcaacta catggtttac

20

<210> 112  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic primer

<400> 112  
gaagatggtg atgggatttc

20

<210> 113  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic probe

<400> 113  
caagcttccc gttctcagcc

20

<210> 114  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic primer

<400> 114  
gggttaccgc tacgaaccgc aggcaggac g

31

<210> 115  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic primer

<400> 115  
cagcctggtc acgtcctggt ctg

23

<210> 116  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic primer

<400> 116  
cagaaggaca tcaactgtga gag

23

<210> 117  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic primer

<400> 117  
gctctagaca gcagatagga ccattcagca g

31

<210> 118  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic primer

<400> 118  
ttgagcggat aaacaggaag gac

23

<210> 119  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic primer

<400> 119  
atctccctgc agttgatgt a gaag

24

<210> 120

<211> 26  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic primer  
  
<400> 120

cgtctggctc aaagagggtc tctatc

26

<210> 121  
<211> 26  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic primer  
  
<400> 121

ctgcggacat agtccctgta ggtttc

26

<210> 122  
<211> 19  
<212> DNA  
<213> Homo sapiens  
  
<400> 122

gtccatgctg gcacacaag

19

<210> 123  
<211> 19  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide  
  
<400> 123

gtccatgcta acacacaag

19

<210> 124  
<211> 21  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic primer  
  
<400> 124

agaggacctg gtgagggata c

21

<210> 125  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic primer

<400> 125  
cttccagaag gcatgttgac

20

<210> 126  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic probe

<400> 126  
cccgtcctca cttgggaacc a

21

<210> 127  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic primer

<400> 127  
cagaaggaca tcaactgtga gag

23

<210> 128  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic primer

<400> 128  
gctctagaca gcagatagga ccattcagca g

31

<210> 129  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic primer

<400> 129  
aactttgcct ttgaagaacc tgag

24

<210> 130  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic primer

<400> 130

acatgaaggt ggggygaacac atag

24

<210> 131

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic primer

<400> 131

atggcagatt catcatcatc atcttc

26

<210> 132

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic primer

<400> 132

tcacccgagc ctctgaatgt tacag

25

<210> 133

<211> 128

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 133

gatccccgaa gagatcaact ggtcggttca agagaccgac cagttgatct cttcttttg

60

gaaagggctt ctcttagttga ccagccacgt tctctggctg gtcaactaga gaagaaaaac

120

cttttagct

128

<210> 134

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic primer

<400> 134

ccgggtacca tggactacaa agacgatgac gataaagggtg gcaggtgggg gcaccat

57

<210> 135

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic primer

<400> 135

atcttotgaa tgcgacagtc cttc

24

<210> 136

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic primer

<400> 136

aaggactgtc gcattcagaa gatc

24

<210> 137

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic primer

<400> 137

ataggatccc caggatcaca tttcaacagt g

31

<210> 138

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic primer

<400> 138

ctgggaaggg cagtcaag

18

<210> 139

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic primer

<400> 139

tgcctctgta tccttgagtc

20

<210> 140

<211> 24

<212> DNA

<213> Artificial Sequence

```

<220>
<223> Synthetic probe

<400> 140
ccgcaggcc ctggatagga cacc                                24

<210> 141
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic primer

<400> 141
tgctacaagt ccgggacaaa                                20

<210> 142
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic primer

<400> 142
gcccagttct gggtcattt                                19

<210> 143
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic probe

<400> 143
cagcagagcc tcagagtgct tcg                                23

<210> 144
<211> 19
<212> DNA
<213> Homo sapiens

<400> 144
ggagatcccg gtggaccac                                19

<210> 145
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

```

<400> 145  
ggagatcctg gtggaccac

19

<210> 146  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic primer

<400> 146  
ggcatatcac agtgggattc

20

<210> 147  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic primer

<400> 147  
gatttcgct gcgatcaac

19

<210> 148  
<211> 2934  
<212> DNA  
<213> Mus musculus

<400> 148  
atggcaagca cccgctgcaa gctggccagg tacctggagg acctggagga tgtggacttg 60  
aagaaaattta agatgcactt agaggactat cctccccaga agggctgcat ccccctcccg 120  
aggggtcaga cagagaaggc agaccatgtg gatctagcca cgctaattatcg ctgacttcaat 180  
ggggaggaga aggcggtggc catggccgtg tggatcttcg ctgcgtcaaa caggagagac 240  
ctttatgaga aagaaaaag agatgagccg aagtgggtt cagataatgc acgtgtttcg 300  
aatcccaactg tgatatgccca ggaagacagc attgaagagg agtggatggg tttactggag 360  
tacctttcga gaatctctat ttgtaaaatg aagaaaagatt accgtaagaa gtacagaaaag 420  
tacgtgagaa gcagattcca gtgcattgaa gacaggaatg cccgtctggg tgagagtgtg 480  
agcctcaaca aacgctacac acgactgcgt ctcataagg agcacccggag ccagcaggag 540  
agggagcagg agcttctggc catcgcaag accaagacgt gtgagagccc cgtgagtccc 600  
attaagatgg agttgctgtt tgaccccgat gatgagcatt ctgagcctgt gcacaccgtg 660  
gtgttccagg gggcgccagg gattggaaa acaatcctgg ccaggaagat gatgttggac 720  
tgggcgtcgg ggacactcta ccaagacagg tttgactatc tgttctatat ccactgtcgg 780  
gaggtgagcc ttgtgacaca gaggagcctg ggggacctga tcatgagctg ctgccccgac 840

ccaaacccac	ccatccacaa	gatcgtgaga	aaaccctcca	gaatcctt	cctcatggac	900
ggcttcgatg	agctgcaagg	tgccttgac	gagcacatag	gaccgctctg	caactgactgg	960
cagaaggccg	agcgaaaa	catttcctg	agcagcctca	tcagaaaagaa	gctgcttccc	1020
gaggcctctc	tgctcatcac	cacgagacct	gtggccctgg	agaaaactgca	gcacttgctg	1080
gaccatcctc	ggcatgtgga	gatcctgggt	ttctccgagg	ccaaaaggaa	agagtacttc	1140
ttcaagtact	tctctgtatga	ggcccaagcc	agggcagcct	tcagtctgat	tcaggagaac	1200
gaggtcctct	tcaccatgtg	cttcatcccc	ctggctgtct	ggatcgtgtg	caactggactg	1260
aaacagcaga	tggagagtgg	caagagcctt	gcccagacat	ccaagaccac	caccgcggtg	1320
tacltcttct	tcctttccag	tttgctgcag	ccccggggag	ggagccagga	gcacggcctc	1380
tgcgccacc	tctgggggct	ctgctcttgc	gctgcagatg	gaatctggaa	ccagaaaatc	1440
ctgtttgagg	agtccgaccc	caggaatcat	ggactgcaga	aggcggatgt	gtctgtttc	1500
ctgaggatga	acctgttcca	aaaggaagtg	gactgcgaga	agttctacag	cttcatccac	1560
atgactttcc	aggagttctt	tgccgccatg	tactacctgc	tggaaagagga	aaaggaagga	1620
aggacgaacg	ttccagggag	tcgtttgaag	cttcccagcc	gagacgtgac	agtccttctg	1680
gaaaactatg	gcaaattcga	aaaggggtat	ttgattttg	ttgtacgttt	cctctttggc	1740
ctggtaaacc	aggagaggac	ctcctacttg	gagaagaaat	taagttgcaa	gatctctcag	1800
caaataaggc	tggagctgct	gaaatggatt	gaagtgaaag	ccaaagctaa	aaagctgcag	1860
atccagccca	gccagctgga	attgttctac	tgtttgtacg	agatgcagga	ggaggacttc	1920
gtgcaaagg	ccatggacta	tttccccaa	attgagatca	atctctccac	cagaatggac	1980
cacatggttt	cttccttttgc	cattgagaac	tgtcatcggt	tggagtca	gtccctgggg	2040
tttctccata	acatgccc	ggaggaagag	gaggagaaa	aggaaggccg	acaccttgc	2100
atgggcagt	gtgtcctccc	aagctcctct	catgctgcct	gttctcatgg	gttggggcgc	2160
tgtggcctct	cgcattgatg	ctgcttcgac	atctccttgc	tcctcagcag	caaccagaag	2220
ctgggtggagc	tggacctgag	tgacaacgccc	ctcggtgact	tcggaatcag	acttctgtgt	2280
gtgggactga	agcacctgtt	gtgcaatctg	aagaagctct	ggttggtcag	ctgctgcctc	2340
acatcagcat	gttgcagga	tcttgcata	gtattgagca	ccagccattc	cctgaccaga	2400
ctctatgtgg	gggagaatgc	cttggagac	tcaggagtcg	caattttatg	tgaaaaagcc	2460
aagaatccac	agtgtaacct	gcagaaaactg	gggttgggtga	attctggcct	tacgtcagtc	2520
tgttggtcag	ctttgtcctc	ggtactcagc	actaatcaga	atctcacgca	cctttacctg	2580
cgaggcaaca	ctctcgagaa	caaggggatc	aaactactct	gtgagggact	cttgcaccc	2640

gactgcaagc ttcaggtgtt ggaatttagac aactgcaacc tcacgtcaca ctgctgctgg 2700  
gatctttcca cacttctgac ctccagccag agcctgcgaa agctgagcct gggcaacaat 2760  
gacctggcg acctgggggt catgatgttc tgtgaagtgc tgaaacagca gagctgcctc 2820  
ctgcagaacc tggggttgtc tgaaatgtat ttcaattatg agacaaaaag tgcgttagaa 2880  
acacttcaag aagaaaagcc tgagctgacc gtcgtcttg agccttcttg gtag 2934

<210> 149

<211> 977

<212> PRT

<213> Mus musculus

<400> 149

Met Ala Ser Thr Arg Cys Lys Leu Ala Arg Tyr Leu Glu Asp Leu Glu  
1 5 10 15

Asp Val Asp Leu Lys Lys Phe Lys Met His Leu Glu Asp Tyr Pro Pro  
20 25 30

Gln Lys Gly Cys Ile Pro Leu Pro Arg Gly Gln Thr Glu Lys Ala Asp  
35 40 45

His Val Asp Leu Ala Thr Leu Met Ile Asp Phe Asn Gly Glu Glu Lys  
50 55 60

Ala Trp Ala Met Ala Val Trp Ile Phe Ala Ala Ile Asn Arg Arg Asp  
65 70 75 80

Leu Tyr Glu Lys Ala Lys Arg Asp Glu Pro Lys Trp Gly Ser Asp Asn  
85 90 95

Ala Arg Val Ser Asn Pro Thr Val Ile Cys Gln Glu Asp Ser Ile Glu  
100 105 110

Glu Glu Trp Met Gly Leu Leu Glu Tyr Leu Ser Arg Ile Ser Ile Cys  
115 120 125

Lys Met Lys Lys Asp Tyr Arg Lys Lys Tyr Arg Lys Tyr Val Arg Ser  
130 135 140

Arg Phe Gln Cys Ile Glu Asp Arg Asn Ala Arg Leu Gly Glu Ser Val  
145 150 155 160

Ser Leu Asn Lys Arg Tyr Thr Arg Leu Arg Leu Ile Lys Glu His Arg  
165 170 175

Ser Gln Gln Glu Arg Glu Gln Glu Leu Leu Ala Ile Gly Lys Thr Lys  
180 185 190

Thr Cys Glu Ser Pro Val Ser Pro Ile Lys Met Glu Leu Leu Phe Asp  
195 200 205

Pro Asp Asp Glu His Ser Glu Pro Val His Thr Val Val Phe Gln Gly  
210 215 220

Ala Ala Gly Ile Gly Lys Thr Ile Leu Ala Arg Lys Met Met Leu Asp  
225 230 235 240

Trp Ala Ser Gly Thr Leu Tyr Gln Asp Arg Phe Asp Tyr Leu Phe Tyr  
245 250 255

Ile His Cys Arg Glu Val Ser Leu Val Thr Gln Arg Ser Leu Gly Asp  
260 265 270

Leu Ile Met Ser Cys Cys Pro Asp Pro Asn Pro Pro Ile His Lys Ile  
275 280 285

Val Arg Lys Pro Ser Arg Ile Leu Phe Leu Met Asp Gly Phe Asp Glu  
290 295 300

Leu Gln Gly Ala Phe Asp Glu His Ile Gly Pro Leu Cys Thr Asp Trp  
305 310 315 320

Gln Lys Ala Glu Arg Gly Asp Ile Leu Leu Ser Ser Leu Ile Arg Lys  
325 330 335

Lys Leu Leu Pro Glu Ala Ser Leu Leu Ile Thr Thr Arg Pro Val Ala  
340 345 350

Leu Glu Lys Leu Gln His Leu Leu Asp His Pro Arg His Val Glu Ile  
355 360 365

Leu Gly Phe Ser Glu Ala Lys Arg Lys Glu Tyr Phe Phe Lys Tyr Phe  
370 375 380

Ser Asp Glu Ala Gln Ala Arg Ala Ala Phe Ser Leu Ile Gln Glu Asn  
385 390 395 400

Glu Val Leu Phe Thr Met Cys Phe Ile Pro Leu Val Cys Trp Ile Val  
405 410 415

Cys Thr Gly Leu Lys Gln Gln Met Glu Ser Gly Lys Ser Leu Ala Gln  
420 425 430

Thr Ser Lys Thr Thr Ala Val Tyr Val Phe Phe Leu Ser Ser Leu  
435 440 445

Leu Gln Pro Arg Gly Gly Ser Gln Glu His Gly Leu Cys Ala His Leu  
450 455 460

Trp Gly Leu Cys Ser Leu Ala Ala Asp Gly Ile Trp Asn Gln Lys Ile  
465 470 475 480

Leu Phe Glu Glu Ser Asp Leu Arg Asn His Gly Leu Gln Lys Ala Asp  
485 490 495

Val Ser Ala Phe Leu Arg Met Asn Leu Phe Gln Lys Glu Val Asp Cys  
500 505 510

Glu Lys Phe Tyr Ser Phe Ile His Met Thr Phe Gln Glu Phe Ala  
515 520 525

Ala Met Tyr Tyr Leu Leu Glu Glu Lys Glu Gly Arg Thr Asn Val  
530 535 540

Pro Gly Ser Arg Leu Lys Leu Pro Ser Arg Asp Val Thr Val Leu Leu  
545 550 555 560

Glu Asn Tyr Gly Lys Phe Glu Lys Gly Tyr Leu Ile Phe Val Val Arg  
565 570 575

Phe Leu Phe Gly Leu Val Asn Gln Glu Arg Thr Ser Tyr Leu Glu Lys  
580 585 590

Lys Leu Ser Cys Lys Ile Ser Gln Gln Ile Arg Leu Glu Leu Leu Lys  
595 600 605

Trp Ile Glu Val Lys Ala Lys Lys Leu Gln Ile Gln Pro Ser  
610 615 620

Gln Leu Glu Leu Phe Tyr Cys Leu Tyr Glu Met Gln Glu Glu Asp Phe  
625 630 635 640

Val Gln Arg Ala Met Asp Tyr Phe Pro Lys Ile Glu Ile Asn Leu Ser  
645 650 655

Thr Arg Met Asp His Met Val Ser Ser Phe Cys Ile Glu Asn Cys His

660

665

670

Arg Val Glu Ser Leu Ser Leu Gly Phe Leu His Asn Met Pro Lys Glu  
675 680 685

Glu Glu Glu Glu Lys Glu Gly Arg His Leu Asp Met Val Gln Cys  
690 695 700

Val Leu Pro Ser Ser His Ala Ala Cys Ser His Gly Leu Gly Arg  
705 710 715 720

Cys Gly Leu Ser His Glu Cys Cys Phe Asp Ile Ser Leu Val Leu Ser  
725 730 735

Ser Asn Gln Lys Leu Val Glu Leu Asp Leu Ser Asp Asn Ala Leu Gly  
740 745 750

Asp Phe Gly Ile Arg Leu Leu Cys Val Gly Leu Lys His Leu Leu Cys  
755 760 765

Asn Leu Lys Lys Leu Trp Leu Val Ser Cys Cys Leu Thr Ser Ala Cys  
770 775 780

Cys Gln Asp Leu Ala Ser Val Leu Ser Thr Ser His Ser Leu Thr Arg  
785 790 795 800

Leu Tyr Val Gly Glu Asn Ala Leu Gly Asp Ser Gly Val Ala Ile Leu  
805 810 815

Cys Glu Lys Ala Lys Asn Pro Gln Cys Asn Leu Gln Lys Leu Gly Leu  
820 825 830

Val Asn Ser Gly Leu Thr Ser Val Cys Cys Ser Ala Leu Ser Ser Val  
835 840 845

Leu Ser Thr Asn Gln Asn Leu Thr His Leu Tyr Leu Arg Gly Asn Thr  
850 855 860

Leu Gly Asp Lys Gly Ile Lys Leu Leu Cys Glu Gly Leu Leu His Pro  
865 870 875 880

Asp Cys Lys Leu Gln Val Leu Glu Leu Asp Asn Cys Asn Leu Thr Ser  
885 890 895

His Cys Cys Trp Asp Leu Ser Thr Leu Leu Thr Ser Ser Gln Ser Leu  
900 905 910

Arg Lys Leu Ser Leu Gly Asn Asn Asp Leu Gly Asp Leu Gly Val Met  
915 920 925

Met Phe Cys Glu Val Leu Lys Gln Gln Ser Cys Leu Leu Gln Asn Leu  
930 935 940

Gly Leu Ser Glu Met Tyr Phe Asn Tyr Glu Thr Lys Ser Ala Leu Glu  
945 950 955 960

Thr Leu Gln Glu Glu Lys Pro Glu Leu Thr Val Val Phe Glu Pro Ser  
965 970 975

Trp

<210> 150  
<211> 30  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Consensus Motif I

<220>  
<221> MISC\_FEATURE  
<222> (1)..(1)  
<223> "Xaa" denotes any amino acid residue.

<220>  
<221> MISC\_FEATURE  
<222> (6)..(6)  
<223> "Xaa" denotes any amino acid residue.

<220>  
<221> MISC\_FEATURE  
<222> (8)..(8)  
<223> "Xaa" denotes any amino acid residue.

<220>  
<221> MISC\_FEATURE  
<222> (11)..(11)  
<223> "Xaa" denotes a hydrophobic amino acid residue.

<220>  
<221> MISC\_FEATURE  
<222> (18)..(19)  
<223> "Xaa" denotes a basic amino acid residue.

<220>  
<221> MISC\_FEATURE  
<222> (20)..(21)  
<223> "Xaa" denotes a hydrophobic amino acid residue.

```
<220>
<221> MISC_FEATURE
<222> (23)..(23)
<223> "Xaa" denotes any amino acid residue.

<220>
<221> MISC_FEATURE
<222> (26)..(26)
<223> "Xaa" denotes any amino acid residue.

<220>
<221> MISC_FEATURE
<222> (28)..(28)
<223> "Xaa" denotes any amino acid residue.

<220>
<221> MISC_FEATURE
<222> (30)..(30)
<223> "Xaa" denotes an aromatic amino acid residue.

<400> 150

Xaa Thr Val Val Leu Xaa Gly Xaa Ala Gly Xaa Gly Lys Thr Thr Leu
1           5           10          15

Ala Xaa Xaa Xaa Xaa Leu Xaa Trp Ala Xaa Gly Xaa Leu Xaa
20           25           30

<210> 151
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus Motif II

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> "Xaa" denotes any amino acid residue.

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> "Xaa" denotes an aromatic amino acid residue.

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> "Xaa" denotes a hydrophobic amino acid residue.

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> "Xaa" denotes an aromatic amino acid residue.

<220>
<221> MISC_FEATURE
```

```

<222> (7)..(7)
<223> "Xaa" denotes a hydrophobic amino acid residue.

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> "Xaa" denotes any amino acid residue.

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> "Xaa" denotes a basic amino acid residue.

<220>
<221> MISC_FEATURE
<222> (12)..(12)
<223> "Xaa" denotes a hydrophobic amino acid residue.

<220>
<221> MISC_FEATURE
<222> (13)..(18)
<223> "Xaa" denotes any amino acid residue.

<220>
<221> MISC_FEATURE
<222> (20)..(20)
<223> "Xaa" denotes a hydrophobic amino acid residue.

<220>
<221> MISC_FEATURE
<222> (21)..(21)
<223> "Xaa" denotes any amino acid residue.

<220>
<221> MISC_FEATURE
<222> (22)..(22)
<223> "Xaa" denotes an acidic amino acid residue.

<220>
<221> MISC_FEATURE
<222> (25)..(27)
<223> "Xaa" denotes any amino acid residue.

<220>
<221> MISC_FEATURE
<222> (28)..(28)
<223> "Xaa" denotes an aromatic amino acid residue.

<400> 151

Phe Xaa Xaa Xaa Phe Xaa Xaa Xaa Cys Xaa Glu Xaa Xaa Xaa Xaa Xaa
1           5           10          15

Xaa Xaa Ser Xaa Xaa Xaa Leu Leu Xaa Xaa Xaa Xaa Pro
20          25

<210> 152
<211> 19
<212> PRT

```

<213> Artificial Sequence

<220>

<223> Consensus Motif III

<220>

<221> MISC\_FEATURE

<222> (1)..(1)

<223> "Xaa" denotes any amino acid residue.

<220>

<221> MISC\_FEATURE

<222> (3)..(3)

<223> "Xaa" denotes a hydrophobic amino acid residue.

<220>

<221> MISC\_FEATURE

<222> (4)..(5)

<223> "Xaa" denotes any amino acid residue.

<220>

<221> MISC\_FEATURE

<222> (7)..(7)

<223> "Xaa" denotes an acidic amino acid residue.

<220>

<221> MISC\_FEATURE

<222> (13)..(13)

<223> "Xaa" denotes a hydrophobic amino acid residue.

<400> 152

Xaa Leu Xaa Xaa Xaa Pro Xaa Arg Leu Leu Phe Leu Xaa Asp Gly Phe  
1 5 10 15

Asp Glu Leu

<210> 153

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus Motif IV

<220>

<221> MISC\_FEATURE

<222> (3)..(3)

<223> "Xaa" denotes any amino acid residue.

<220>

<221> MISC\_FEATURE

<222> (7)..(7)

<223> "Xaa" denotes a basic amino acid residue.

<220>

<221> MISC\_FEATURE  
<222> (9)..(9)  
<223> "Xaa" denotes any amino acid residue.

<220>  
<221> MISC\_FEATURE  
<222> (20)..(20)  
<223> "Xaa" denotes serine or threonine.

<220>  
<221> MISC\_FEATURE  
<222> (23)..(23)  
<223> "Xaa" denotes any amino acid residue.

<220>  
<221> MISC\_FEATURE  
<222> (25)..(25)  
<223> "Xaa" denotes a hydrophobic amino acid residue.

<400> 153

Leu Leu Xaa Ser Leu Leu Xaa Lys Xaa Leu Leu Pro Glu Ala Ser Leu  
1 5 10 15

Leu Leu Thr Xaa Arg Pro Xaa Ala Xaa  
20 25

<210> 154  
<211> 31  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Consensus Motif V

<220>  
<221> MISC\_FEATURE  
<222> (2)..(3)  
<223> "Xaa" denotes any amino acid residue.

<220>  
<221> MISC\_FEATURE  
<222> (4)..(4)  
<223> "Xaa" denotes a hydrophobic amino acid residue.

<220>  
<221> MISC\_FEATURE  
<222> (6)..(8)  
<223> "Xaa" denotes any amino acid residue.

<220>  
<221> MISC\_FEATURE  
<222> (9)..(9)  
<223> "Xaa" denotes a basic amino acid residue.

<220>  
<221> MISC\_FEATURE  
<222> (10)..(10)

```
<223> "Xaa" denotes any amino acid residue.

<220>
<221> MISC_FEATURE
<222> (11)..(11)
<223> "Xaa" denotes a hydrophobic amino acid residue.

<220>
<221> MISC_FEATURE
<222> (12)..(12)
<223> "Xaa" denotes any amino acid residue.

<220>
<221> MISC_FEATURE
<222> (13)..(13)
<223> "Xaa" denotes a hydrophobic amino acid residue.

<220>
<221> MISC_FEATURE
<222> (14)..(14)
<223> "Xaa" denotes any amino acid residue.

<220>
<221> MISC_FEATURE
<222> (19)..(19)
<223> "Xaa" denotes any amino acid residue.

<220>
<221> MISC_FEATURE
<222> (20)..(20)
<223> "Xaa" denotes an acidic amino acid residue.

<220>
<221> MISC_FEATURE
<222> (21)..(22)
<223> "Xaa" denotes a basic amino acid residue.

<220>
<221> MISC_FEATURE
<222> (23)..(24)
<223> "Xaa" denotes any amino acid residue.

<220>
<221> MISC_FEATURE
<222> (27)..(28)
<223> "Xaa" denotes any amino acid residue.

<220>
<221> MISC_FEATURE
<222> (29)..(29)
<223> "Xaa" denotes an aromatic amino acid residue.

<220>
<221> MISC_FEATURE
<222> (30)..(30)
<223> "Xaa" denotes any amino acid residue.

<220>
<221> MISC_FEATURE
<222> (31)..(31)
<223> "Xaa" denotes an acidic amino acid residue.
```

<400> 154

Leu Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Phe  
1 5 10 15

Ser Glu Xaa Xaa Xaa Xaa Xaa Xaa Tyr Phe Xaa Xaa Xaa Xaa Xaa  
20 25 30

<210> 155

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus Motif VI

<220>

<221> MISC\_FEATURE

<222> (2)..(2)

<223> "Xaa" denotes any amino acid residue.

<220>

<221> MISC\_FEATURE

<222> (3)..(3)

<223> "Xaa" denotes a basic amino acid residue.

<220>

<221> MISC\_FEATURE

<222> (5)..(5)

<223> "Xaa" denotes a hydrophobic amino acid residue.

<220>

<221> MISC\_FEATURE

<222> (6)..(7)

<223> "Xaa" denotes any amino acid residue.

<220>

<221> MISC\_FEATURE

<222> (8)..(8)

<223> "Xaa" denotes a hydrophobic amino acid residue.

<220>

<221> MISC\_FEATURE

<222> (9)..(9)

<223> "Xaa" denotes a basic amino acid residue.

<220>

<221> MISC\_FEATURE

<222> (10)..(10)

<223> "Xaa" denotes any amino acid residue.

<220>

<221> MISC\_FEATURE

<222> (12)..(13)

<223> "Xaa" denotes any amino acid residue.

<220>

```
<221> MISC_FEATURE
<222> (15)..(15)
<223> "Xaa" denotes an aromatic amino acid residue.

<220>
<221> MISC_FEATURE
<222> (16)..(16)
<223> "Xaa" denotes any amino acid residue.

<220>
<221> MISC_FEATURE
<222> (17)..(17)
<223> "Xaa" denotes a hydrophobic amino acid residue.

<220>
<221> MISC_FEATURE
<222> (19)..(19)
<223> "Xaa" denotes any amino acid residue.

<220>
<221> MISC_FEATURE
<222> (22)..(22)
<223> "Xaa" denotes any amino acid residue.

<220>
<221> MISC_FEATURE
<222> (23)..(23)
<223> "Xaa" denotes a hydrophobic amino acid residue.

<220>
<221> MISC_FEATURE
<222> (26)..(26)
<223> "Xaa" denotes a hydrophobic amino acid residue.

<220>
<221> MISC_FEATURE
<222> (29)..(29)
<223> "Xaa" denotes serine or threonine.

<220>
<221> MISC_FEATURE
<222> (30)..(30)
<223> "Xaa" denotes any amino acid residue.

<220>
<221> MISC_FEATURE
<222> (32)..(32)
<223> "Xaa" denotes a basic amino acid residue.

<220>
<221> MISC_FEATURE
<222> (33)..(33)
<223> "Xaa" denotes any amino acid residue.

<220>
<221> MISC_FEATURE
<222> (35)..(35)
<223> "Xaa" denotes a hydrophobic amino acid residue.

<220>
<221> MISC_FEATURE
```

<222> (36)..(36)  
<223> "Xaa" denotes an acidic amino acid residue.

<220>  
<221> MISC\_FEATURE  
<222> (37)..(37)  
<223> "Xaa" denotes any amino acid residue.

<400> 155

Ala Xaa Xaa Ser Xaa Xaa Xaa Xaa Xaa Asn Xaa Xaa Leu Xaa Xaa  
1 5 10 15

Xaa Cys Xaa Val Pro Xaa Xaa Cys Trp Xaa Val Cys Xaa Xaa Leu Xaa  
20 25 30

Xaa Gln Xaa Xaa Xaa Gly  
35

<210> 156  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Consensus Motif VII

<220>  
<221> MISC\_FEATURE  
<222> (2)..(2)  
<223> "Xaa" denotes any amino acid residue.

<220>  
<221> MISC\_FEATURE  
<222> (4)..(4)  
<223> "Xaa" denotes any amino acid residue.

<220>  
<221> MISC\_FEATURE  
<222> (5)..(5)  
<223> "Xaa" denotes a hydrophobic amino acid residue.

<220>  
<221> MISC\_FEATURE  
<222> (6)..(6)  
<223> "Xaa" denotes an aromatic amino acid residue.

<220>  
<221> MISC\_FEATURE  
<222> (7)..(8)  
<223> "Xaa" denotes any amino acid residue.

<220>  
<221> MISC\_FEATURE  
<222> (9)..(9)  
<223> "Xaa" denotes an aromatic amino acid residue.

```
<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> "Xaa" denotes a hydrophobic amino acid residue.

<220>
<221> MISC_FEATURE
<222> (11)..(13)
<223> "Xaa" denotes any amino acid residue.

<220>
<221> MISC_FEATURE
<222> (14)..(14)
<223> "Xaa" denotes a hydrophobic acid residue.

<400> 156

Thr Xaa Thr Xaa Xaa
1           5           10

<210> 157
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus Motif VIII

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> "Xaa" denotes a basic amino acid residue.

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> "Xaa" denotes any amino acid residue.

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> "Xaa" denotes any amino acid residue.

<220>
<221> MISC_FEATURE
<222> (12)..(12)
<223> "Xaa" denotes a hydrophobic amino acid residue.

<220>
<221> MISC_FEATURE
<222> (14)..(17)
<223> "Xaa" denotes any amino acid residue.

<220>
<221> MISC_FEATURE
<222> (18)..(18)
<223> "Xaa" denotes a hydrophobic amino acid residue.

<220>
```

```

<221> MISC_FEATURE
<222> (20)..(21)
<223> "Xaa" denotes any amino acid residue.

<220>
<221> MISC_FEATURE
<222> (22)..(22)
<223> "Xaa" denotes an acidic amino acid residue.

<220>
<221> MISC_FEATURE
<222> (25)..(27)
<223> "Xaa" denotes any amino acid residue.

<220>
<221> MISC_FEATURE
<222> (30)..(33)
<223> "Xaa" denotes any amino acid residue.

<220>
<221> MISC_FEATURE
<222> (34)..(34)
<223> "Xaa" denotes a hydrophobic amino acid residue.

<220>
<221> MISC_FEATURE
<222> (35)..(36)
<223> "Xaa" denotes any amino acid residue.

<220>
<221> MISC_FEATURE
<222> (39)..(41)
<223> "Xaa" denotes any amino acid residue.

<220>
<221> MISC_FEATURE
<222> (42)..(43)
<223> "Xaa" denotes a hydrophobic amino acid residue.

<400> 157

Leu Xaa Xaa Leu Cys Xaa Leu Ala Ala Glu Gly Xaa Trp Xaa Xaa Xaa
1           5           10          15

Xaa Xaa Phe Xaa Xaa Xaa Asp Leu Xaa Xaa Xaa Gly Leu Xaa Xaa Xaa
20          25          30

Xaa Xaa Xaa Xaa Phe Leu Xaa Xaa Xaa Xaa Xaa
35          40

<210> 158
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus Motif IX

```

```
<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> "Xaa" denotes any amino acid residue.

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> "Xaa" denotes a hydrophobic amino acid residue.

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> "Xaa" denotes serine or threonine.

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> "Xaa" denotes a hydrophobic amino acid residue.

<220>
<221> MISC_FEATURE
<222> (12)..(12)
<223> "Xaa" denotes any amino acid residue.

<220>
<221> MISC_FEATURE
<222> (15)..(15)
<223> "Xaa" denotes a hydrophobic amino acid residue.

<220>
<221> MISC_FEATURE
<222> (16)..(16)
<223> "Xaa" denotes an aromatic acid residue.

<220>
<221> MISC_FEATURE
<222> (18)..(18)
<223> "Xaa" denotes a hydrophobic acid residue.
```

<400> 158

Tyr Xaa Phe Xaa His Leu Xaa Xaa Gln Glu Phe Xaa Ala Ala Xaa Xaa  
1 5 10 15

Tyr Xaa Leu

```
<210> 159
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus Motif X
```

<220>

```
<221> MISC_FEATURE
<222> (7)..(7)
<223> "Xaa" denotes any amino acid residue.

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> "Xaa" denotes any amino acid residue and is varialble in length.

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> "Xaa" denotes any amino acid residue.

<220>
<221> MISC_FEATURE
<222> (11)..(11)
<223> "Xaa" denotes a basic amino acid residue.

<220>
<221> MISC_FEATURE
<222> (12)..(12)
<223> "Xaa" denotes any amino acid residue.

<220>
<221> MISC_FEATURE
<222> (15)..(16)
<223> "Xaa" denotes any amino acid residue.

<220>
<221> MISC_FEATURE
<222> (19)..(20)
<223> "Xaa" denotes any amino acid residue.

<220>
<221> MISC_FEATURE
<222> (21)..(21)
<223> "Xaa" denotes a hydrophobic amino acid residue.

<220>
<221> MISC_FEATURE
<222> (23)..(24)
<223> "Xaa" denotes any amino acid residue.

<220>
<221> MISC_FEATURE
<222> (25)..(25)
<223> "Xaa" denotes a hydrophobic amino acid residue.

<220>
<221> MISC_FEATURE
<222> (26)..(26)
<223> "Xaa" denotes a basic amino acid residue.

<400> 159
```

Phe Leu Phe Gly Leu Leu Xaa Xaa Asn Xaa Xaa Xaa Leu Glu Xaa Xaa  
1 5 10 15

Phe Ser Xaa Xaa Xaa Ser Xaa Xaa Xaa Xaa

```
<210> 160
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus Motif XI

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> "Xaa" denotes a hydrophobic amino acid residue.

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> "Xaa" denotes an acidic amino acid residue.

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> "Xaa" denotes any amino acid residue.

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> "Xaa" denotes an aromatic amino acid residue.

<220>
<221> MISC_FEATURE
<222> (9)..(9)
<223> "Xaa" denotes an acidic amino acid residue.

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> "Xaa" denotes any amino acid residue.

<220>
<221> MISC_FEATURE
<222> (13)..(13)
<223> "Xaa" denotes any amino acid residue.

<220>
<221> MISC_FEATURE
<222> (14)..(14)
<223> "Xaa" denotes an acidic amino acid residue.

<220>
<221> MISC_FEATURE
<222> (16)..(16)
<223> "Xaa" denotes a hydrophobic amino acid residue.

<220>
<221> MISC_FEATURE
<222> (17)..(19)
<223> "Xaa" denotes any amino acid residue.
```

<220>  
<221> MISC\_FEATURE  
<222> (20)..(20)  
<223> "Xaa" denotes a hydrophobic amino acid residue.

<220>  
<221> MISC\_FEATURE  
<222> (21)..(25)  
<223> "Xaa" denotes any amino acid residue.

<220>  
<221> MISC\_FEATURE  
<222> (26)..(26)  
<223> "Xaa" denotes a hydrophobic amino acid residue.

<220>  
<221> MISC\_FEATURE  
<222> (27)..(27)  
<223> "Xaa" denotes any amino acid residue.

<220>  
<221> MISC\_FEATURE  
<222> (28)..(28)  
<223> "Xaa" denotes a hydrophobic amino acid residue.

<400> 160

Xaa Xaa Leu Phe Xaa Cys Leu Arg Ala Xaa Gln Glu Xaa Ala Phe His  
1 5 10 15

Xaa Xaa Xaa His Xaa Xaa Xaa Xaa His Xaa His  
20 25

<210> 161  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Consensus Motif XII

<220>  
<221> MISC\_FEATURE  
<222> (1)..(1)  
<223> "Xaa" denotes an acidic amino acid residue.

<220>  
<221> MISC\_FEATURE  
<222> (2)..(3)  
<223> "Xaa" denotes a hydrophobic amino acid residue.

<220>  
<221> MISC\_FEATURE  
<222> (5)..(5)  
<223> "Xaa" denotes any amino acid residue.

<220>

<221> MISC\_FEATURE  
<222> (6)..(6)  
<223> "Xaa" denotes serine or threonine.

<220>  
<221> MISC\_FEATURE  
<222> (10)..(11)  
<223> "Xaa" denotes a basic amino acid residue.

<220>  
<221> MISC\_FEATURE  
<222> (13)..(14)  
<223> "Xaa" denotes any amino acid residue.

<220>  
<221> MISC\_FEATURE  
<222> (15)..(15)  
<223> "Xaa" denotes a hydrophobic amino acid residue.

<220>  
<221> MISC\_FEATURE  
<222> (16)..(17)  
<223> "Xaa" denotes any amino acid residue.

<220>  
<221> MISC\_FEATURE  
<222> (19)..(19)  
<223> "Xaa" denotes any amino acid residue.

<400> 161

Xaa Xaa Xaa Val Xaa Xaa Phe Cys Leu Xaa Xaa Cys Xaa Xaa Xaa Xaa  
1 5 10 15

Xaa Leu Xaa Leu  
20

<210> 162  
<211> 479  
<212> PRT  
<213> Homo sapiens

<400> 162

Met Glu Leu Leu Phe Asp Pro Asp Asp Glu His Ser Glu Pro Val His  
1 5 10 15

Thr Val Val Phe Gln Gly Ala Ala Gly Ile Gly Lys Thr Ile Leu Ala  
20 25 30

Arg Lys Met Met Leu Asp Trp Ala Ser Gly Thr Leu Tyr Gln Asp Arg  
35 40 45

Phe Asp Tyr Leu Phe Tyr Ile His Cys Arg Glu Val Ser Leu Val Thr  
50 55 60

Gln Arg Ser Leu Gly Asp Leu Ile Met Ser Cys Cys Pro Asp Pro Asn  
65 70 75 80

Pro Pro Ile His Lys Ile Val Arg Lys Pro Ser Arg Ile Leu Phe Leu  
85 90 95

Met Asp Gly Phe Asp Glu Leu Gln Gly Ala Phe Asp Glu His Ile Gly  
100 105 110

Pro Leu Cys Thr Asp Trp Gln Lys Ala Glu Arg Gly Asp Ile Leu Leu  
115 120 125

Ser Ser Leu Ile Arg Lys Lys Leu Leu Pro Glu Ala Ser Leu Leu Ile  
130 135 140

Thr Thr Arg Pro Val Ala Leu Glu Lys Leu Gln His Leu Leu Asp His  
145 150 155 160

Pro Arg His Val Glu Ile Leu Gly Phe Ser Glu Ala Lys Arg Lys Glu  
165 170 175

Tyr Phe Phe Lys Tyr Phe Ser Asp Glu Ala Gln Ala Arg Ala Ala Phe  
180 185 190

Ser Leu Ile Gln Glu Asn Glu Val Leu Phe Thr Met Cys Phe Ile Pro  
195 200 205

Leu Val Cys Trp Ile Val Cys Thr Gly Leu Lys Gln Gln Met Glu Ser  
210 215 220

Gly Lys Ser Leu Ala Gln Thr Ser Lys Thr Ser Thr Ala Val Tyr Val  
225 230 235 240

Phe Phe Leu Ser Ser Leu Leu Gln Pro Arg Gly Gly Ser Gln Glu His  
245 250 255

Gly Leu Cys Ala His Leu Trp Gly Leu Cys Ser Leu Ala Ala Asp Gly  
260 265 270

Ile Trp Asn Gln Lys Ile Leu Phe Glu Glu Ser Asp Leu Arg Asn His  
275 280 285

Gly Leu Gln Lys Ala Asp Val Ser Ala Phe Leu Arg Met Asn Leu Phe  
290 295 300

Gln Lys Glu Val Asp Cys Glu Lys Phe Tyr Ser Phe Ile His Met Thr  
305 310 315 320

Phe Gln Glu Phe Phe Ala Ala Met Tyr Tyr Leu Leu Glu Glu Lys  
325 330 335

Glu Gly Arg Thr Asn Val Pro Gly Ser Arg Leu Lys Leu Pro Ser Arg  
340 345 350

Asp Val Thr Val Leu Leu Glu Asn Tyr Gly Lys Phe Glu Lys Gly Tyr  
355 360 365

Leu Ile Phe Val Val Arg Phe Leu Phe Gly Leu Val Asn Gln Glu Arg  
370 375 380

Thr Ser Tyr Leu Glu Lys Lys Leu Ser Cys Met Ile Ser Gln Gln Ile  
385 390 395 400

Arg Leu Glu Leu Leu Lys Trp Ile Glu Val Lys Ala Lys Ala Lys Lys  
405 410 415

Leu His Asp Gln Pro Ser Gln Leu Glu Leu Phe Tyr Cys Leu Tyr Glu  
420 425 430

Met Gln Glu Glu Asp Phe Val Gln Arg Ala Met Asp Tyr Phe Pro Lys  
435 440 445

Ile Glu Ile Asn Leu Ser Thr Arg Met Asp His Met Val Ser Ser Phe  
450 455 460

Cys Ile Glu Asn Cys His Arg Val Glu Ser Leu Ser Leu Gly Phe  
465 470 475

<210> 163  
<211> 472  
<212> PRT  
<213> Homo sapiens

<400> 163

Ile Glu Thr Leu Phe Glu Pro Asp Glu Glu Arg Pro Glu Pro Pro Arg  
1 5 10 15

Thr Val Val Met Gln Gly Ala Ala Gly Ile Gly Lys Ser Met Leu Ala  
20 25 30

His Lys Val Met Leu Asp Trp Ala Asp Gly Lys Leu Phe Gln Gly Arg  
35 40 45

Phe Asp Tyr Leu Phe Tyr Ile Asn Cys Arg Glu Met Asn Gln Ser Ala  
50 55 60

Thr Glu Cys Ser Met Gln Asp Leu Ile Phe Ser Cys Trp Pro Glu Pro  
65 70 75 80

Ser Ala Pro Leu Gln Glu Leu Ile Arg Val Pro Glu Arg Leu Leu Phe  
85 90 95

Ile Ile Asp Gly Phe Asp Glu Leu Lys Pro Ser Phe His Asp Pro Gln  
100 105 110

Gly Pro Trp Cys Leu Cys Trp Glu Glu Lys Arg Pro Thr Glu Leu Leu  
115 120 125

Leu Asn Ser Leu Ile Arg Lys Lys Leu Leu Pro Glu Leu Ser Leu Leu  
130 135 140

Ile Thr Thr Arg Pro Thr Ala Leu Glu Lys Leu His Arg Leu Leu Glu  
145 150 155 160

His Pro Arg His Val Glu Ile Leu Gly Phe Ser Glu Ala Glu Arg Lys  
165 170 175

Glu Tyr Phe Tyr Lys Tyr Phe His Asn Ala Glu Gln Ala Gly Gln Val  
180 185 190

Phe Asn Tyr Val Arg Asp Asn Glu Pro Leu Phe Thr Met Cys Phe Val  
195 200 205

Pro Leu Val Cys Trp Val Val Cys Thr Cys Leu Gln Gln Gln Leu Glu  
210 215 220

Gly Gly Gly Leu Leu Arg Gln Thr Ser Arg Thr Thr Thr Ala Val Tyr  
225 230 235 240

Met Leu Tyr Leu Leu Ser Leu Met Gln Pro Lys Pro Gly Ala Pro Arg  
245 250 255

Leu Gln Pro Pro Pro Asn Gln Arg Gly Leu Cys Ser Leu Ala Ala Asp  
260 265 270

Gly Leu Trp Asn Gln Lys Ile Leu Phe Glu Glu Gln Asp Leu Arg Lys  
275 280 285

His Gly Leu Asp Gly Glu Asp Val Ser Ala Phe Leu Asn Met Asn Ile  
290 295 300

Phe Gln Lys Asp Ile Asn Cys Glu Arg Tyr Tyr Ser Phe Ile His Leu  
305 310 315 320

Ser Phe Gln Glu Phe Phe Ala Ala Met Tyr Tyr Ile Leu Asp Glu Gly  
325 330 335

Glu Gly Gly Ala Gly Pro Asp Gln Asp Val Thr Arg Leu Leu Thr Glu  
340 345 350

Tyr Ala Phe Ser Glu Arg Ser Phe Leu Ala Leu Thr Ser Arg Phe Leu  
355 360 365

Phe Gly Leu Leu Asn Glu Glu Thr Arg Ser His Leu Glu Lys Ser Leu  
370 375 380

Cys Trp Lys Val Ser Pro His Ile Lys Met Asp Leu Leu Gln Trp Ile  
385 390 395 400

Gln Ser Lys Ala Gln Ser Asp Gly Ser Thr Leu Gln Gln Gly Ser Leu  
405 410 415

Glu Phe Phe Ser Cys Leu Tyr Glu Ile Gln Glu Glu Glu Phe Ile Gln  
420 425 430

Gln Ala Leu Ser His Phe Gln Val Ile Val Val Ser Asn Ile Ala Ser  
435 440 445

Lys Met Glu His Met Val Ser Ser Phe Cys Leu Lys Arg Cys Arg Ser  
450 455 460

Ala Gln Val Leu His Leu Tyr Gly  
465 470

<210> 164  
<211> 468  
<212> PRT  
<213> Homo sapiens  
  
<400> 164

Glu Tyr Lys Glu Leu Asn Asp Ala Tyr Thr Ala Ala Ala Arg Arg His  
1 5 10 15

Thr Val Val Leu Glu Gly Pro Asp Gly Ile Gly Lys Thr Thr Leu Leu

20

25

30

Arg Lys Val Met Leu Asp Trp Ala Glu Gly Asn Leu Trp Lys Asp Arg  
 35                           40                           45

Phe Thr Phe Val Phe Phe Leu Asn Val Cys Glu Met Asn Gly Ile Ala  
 50                           55                           60

Glu Thr Ser Leu Leu Glu Leu Leu Ser Arg Asp Trp Pro Glu Ser Ser  
 65                           70                           75                           80

Glu Lys Ile Glu Asp Ile Phe Ser Gln Pro Glu Arg Ile Leu Phe Ile  
 85                           90                           95

Met Asp Gly Phe Glu Gln Leu Lys Phe Asn Leu Gln Leu Lys Ala Asp  
 100                        105                           110

Leu Ser Asp Asp Trp Arg Gln Arg Gln Pro Met Pro Ile Ile Leu Ser  
 115                        120                           125

Ser Leu Leu Gln Lys Lys Met Leu Pro Glu Ser Ser Leu Leu Ile Ala  
 130                        135                           140

Leu Gly Lys Leu Ala Met Gln Lys His Tyr Phe Met Leu Arg His Pro  
 145                        150                           155                           160

Lys Leu Ile Lys Leu Leu Gly Phe Ser Glu Ser Glu Lys Lys Ser Tyr  
 165                        170                           175

Phe Ser Tyr Phe Phe Gly Glu Lys Ser Lys Ala Leu Lys Val Phe Asn  
 180                        185                           190

Phe Val Arg Asp Asn Gly Pro Leu Phe Ile Leu Cys His Asn Pro Phe  
 195                        200                           205

Thr Cys Trp Leu Val Cys Thr Cys Val Lys Gln Arg Leu Glu Arg Gly  
 210                        215                           220

Glu Asp Leu Glu Ile Asn Ser Gln Asn Thr Thr Tyr Leu Tyr Ala Ser  
 225                        230                           235                           240

Phe Leu Thr Thr Val Phe Lys Ala Gly Ser Gln Ser Phe Pro Pro Lys  
 245                        250                           255

Val Asn Arg Ala Arg Leu Lys Ser Leu Cys Ala Leu Ala Ala Glu Gly  
 260                        265                           270

Ile Trp Thr Tyr Thr Phe Val Phe Ser His Gly Asp Leu Arg Arg Asn  
275 280 285

Gly Leu Ser Glu Ser Glu Gly Val Met Trp Val Gly Met Arg Leu Leu  
290 295 300

Gln Arg Arg Gly Asp Cys Phe Ala Phe Met His Leu Cys Ile Gln Glu  
305 310 315 320

Phe Cys Ala Ala Met Phe Tyr Leu Leu Lys Arg Pro Lys Asp Asp Pro  
325 330 335

Asn Pro Ala Ile Gly Ser Ile Thr Gln Leu Val Arg Ala Ser Val Val  
340 345 350

Gln Pro Gln Thr Leu Leu Thr Gln Val Gly Ile Phe Met Phe Gly Ile  
355 360 365

Ser Thr Glu Glu Ile Val Ser Met Leu Glu Thr Ser Phe Gly Phe Pro  
370 375 380

Leu Ser Lys Asp Leu Lys Gln Glu Ile Thr Gln Cys Leu Glu Ser Leu  
385 390 395 400

Ser Gln Cys Glu Ala Asp Arg Glu Ala Ile Ala Phe Gln Glu Leu Phe  
405 410 415

Ile Gly Leu Phe Glu Thr Gln Glu Lys Glu Phe Val Thr Lys Val Met  
420 425 430

Asn Phe Phe Glu Glu Val Phe Ile Tyr Ile Gly Asn Ile Glu His Leu  
435 440 445

Val Ile Ala Ser Phe Cys Leu Lys His Cys Gln His Leu Thr Thr Leu  
450 455 460

Arg Met Cys Val  
465

<210> 165  
<211> 297  
<212> PRT  
<213> Homo sapiens

<220>

<221> MISC\_FEATURE  
<222> (74)...(74)  
<223> "Xaa" denotes any amino acid residue.

<220>  
<221> MISC\_FEATURE  
<222> (136)...(136)  
<223> "Xaa" denotes any amino acid residue.

<220>  
<221> MISC\_FEATURE  
<222> (232)...(232)  
<223> "Xaa" denotes any amino acid residue.

<400> 165

His Phe Phe Pro Gln Pro Glu Gln Ile Leu Phe Ile Met Asp Gly Phe  
1 5 10 15

Glu Gln Leu Lys Phe Asp Leu Glu Leu Lys Ala Asp Leu Cys Asp Asp  
20 25 30

Trp Arg Gln Gln Gln Pro Thr Gln Ile Ile Leu Ser Ser Leu Leu Gln  
35 40 45

Lys Lys Met Ile Pro Glu Ser Ser Leu Leu Ile Ala Leu Gly Lys Val  
50 55 60

Gly Met Gln Lys Asn Tyr Phe Met Leu Xaa His Pro Lys Leu Ile Lys  
65 70 75 80

Leu Pro Gly Phe Thr Glu Leu Glu Arg Lys Leu Tyr Phe Ser Tyr Phe  
85 90 95

Phe Ser Glu Lys Asn Thr Phe Ile His Leu Leu Lys Met Asn Ala Ser  
100 105 110

Phe Leu Thr Asn Val Phe Lys Ala Gly Ser Gln Ser Phe Pro Pro Lys  
115 120 125

Gly Met Lys Leu Leu Gln Arg Xaa Gly Glu Cys Phe Thr Phe Ile His  
130 135 140

Val Cys Ile Gln Glu Phe Cys Ala Thr Met Phe Tyr Leu Leu Lys Arg  
145 150 155 160

Pro Lys Asp Asp Pro Asn Pro Thr Ile Gly Ser Ile Thr Gln Leu Val  
165 170 175

Arg Ala Ser Val Ala Gln Pro Gln Thr His Ser Thr Gln Val Gly Val

180

185

190

Phe Val Phe Gly Ile Ser Thr Glu Glu Ile Ile Ser Leu Leu Glu Thr  
195 200 205

Ser Phe Gly Phe Pro Leu Leu Lys Asp Leu Lys Lys Glu Ile Thr Gln  
210 215 220

Cys Leu Lys Ser Leu Ser Gln Xaa Glu Ala Asp Arg Glu Val Ile Gly  
225 230 235 240

Phe Gln Glu Leu Phe His Asp Leu Phe Ala Thr Gln Glu Lys Glu Phe  
245 250 255

Val Thr Glu Val Ile Asn Phe Phe Glu Glu Val Phe Ile Cys Thr Gly  
260 265 270

Asn Ile Glu His Leu Val Val Ser Ser Phe Cys Arg Lys His Cys Gln  
275 280 285

Asn Leu Thr Thr Leu Arg Met Cys Val  
290 295

<210> 166  
<211> 458  
<212> PRT  
<213> Homo sapiens

<400> 166

Ile Arg Asp Leu Phe Gly Pro Gly Leu Asp Thr Gln Glu Pro Arg Ile  
1 5 10 15

Val Ile Leu Gln Gly Ala Ala Gly Ile Gly Lys Ser Thr Leu Ala Arg  
20 25 30

Gln Val Lys Glu Ala Trp Gly Arg Gly Gln Leu Tyr Gly Asp Arg Phe  
35 40 45

Gln His Val Phe Tyr Phe Ser Cys Arg Glu Leu Ala Gln Ser Lys Val  
50 55 60

Val Ser Leu Ala Glu Leu Ile Gly Lys Asp Gly Thr Ala Thr Pro Ala  
65 70 75 80

Pro Ile Arg Gln Ile Leu Ser Arg Pro Glu Arg Leu Leu Phe Ile Leu  
85 90 95

Asp Gly Val Asp Glu Pro Gly Trp Val Leu Gln Glu Pro Ser Ser Glu  
100 105 110

Leu Cys Leu His Trp Ser Gln Pro Gln Pro Ala Asp Ala Leu Leu Gly  
115 120 125

Ser Leu Leu Gly Lys Thr Ile Leu Pro Glu Ala Ser Phe Leu Ile Thr  
130 135 140

Ala Arg Thr Thr Ala Leu Gln Asn Leu Ile Pro Ser Leu Glu Gln Ala  
145 150 155 160

Arg Trp Val Glu Val Leu Gly Phe Ser Glu Ser Ser Arg Lys Glu Tyr  
165 170 175

Phe Tyr Arg Tyr Phe Thr Asp Glu Arg Gln Ala Ile Arg Ala Phe Arg  
180 185 190

Leu Val Lys Ser Asn Lys Glu Leu Trp Ala Leu Cys Leu Val Pro Trp  
195 200 205

Val Ser Trp Leu Ala Cys Thr Cys Leu Met Gln Gln Met Lys Arg Lys  
210 215 220

Glu Lys Leu Thr Leu Thr Ser Lys Thr Thr Thr Thr Leu Cys Leu His  
225 230 235 240

Tyr Leu Ala Gln Ala Leu Gln Ala Gln Pro Leu Gly Pro Gln Leu Arg  
245 250 255

Asp Leu Cys Ser Leu Ala Ala Glu Gly Ile Trp Gln Lys Lys Thr Leu  
260 265 270

Phe Ser Pro Asp Asp Leu Arg Lys His Gly Leu Asp Gly Ala Ile Ile  
275 280 285

Ser Thr Phe Leu Lys Met Gly Ile Leu Gln Glu His Pro Ile Pro Leu  
290 295 300

Ser Tyr Ser Phe Ile His Leu Cys Phe Gln Glu Phe Phe Ala Ala Met  
305 310 315 320

Ser Tyr Val Leu Glu Asp Glu Lys Gly Arg Gly Lys His Ser Asn Cys  
325 330 335

Ile Ile Asp Leu Glu Lys Thr Leu Glu Ala Tyr Gly Ile His Gly Leu  
340 345 350

Phe Gly Ala Ser Thr Thr Arg Phe Leu Leu Gly Leu Leu Ser Asp Glu  
355 360 365

Gly Glu Arg Glu Met Glu Asn Ile Phe His Cys Arg Leu Ser Gln Gly  
370 375 380

Arg Asn Leu Met Gln Trp Val Pro Ser Leu Gln Leu Leu Leu Gln Pro  
385 390 395 400

His Ser Leu Glu Ser Leu His Cys Leu Tyr Glu Thr Arg Asn Lys Thr  
405 410 415

Phe Leu Thr Gln Val Met Ala His Phe Glu Glu Met Gly Met Cys Val  
420 425 430

Glu Thr Asp Met Glu Leu Leu Val Cys Thr Phe Cys Ile Lys Phe Ser  
435 440 445

Arg His Val Lys Lys Leu Gln Leu Ile Glu  
450 455

<210> 167  
<211> 474  
<212> PRT  
<213> Homo sapiens

<400> 167

Leu Glu His Leu Phe Asp Val Asp Val Lys Thr Gly Ala Gln Pro Gln  
1 5 10 15

Ile Val Val Leu Gln Gly Ala Ala Gly Val Gly Lys Thr Thr Leu Val  
20 25 30

Arg Lys Ala Met Leu Asp Trp Ala Glu Gly Ser Leu Tyr Gln Gln Arg  
35 40 45

Phe Lys Tyr Val Phe Tyr Leu Asn Gly Arg Glu Ile Asn Gln Leu Lys  
50 55 60

Glu Arg Ser Phe Ala Gln Leu Ile Ser Lys Asp Trp Pro Ser Thr Glu  
65 70 75 80

Gly Pro Ile Glu Glu Ile Met Tyr Gln Pro Ser Ser Leu Leu Phe Ile  
85 90 95

Ile Asp Ser Phe Asp Glu Leu Asn Phe Ala Phe Glu Glu Pro Glu Phe  
100 105 110

Ala Leu Cys Glu Asp Trp Thr Gln Glu His Pro Val Ser Phe Leu Met  
115 120 125

Ser Ser Leu Leu Arg Lys Val Met Leu Pro Glu Ala Ser Leu Leu Val  
130 135 140

Thr Thr Arg Leu Thr Thr Ser Lys Arg Leu Lys Gln Leu Leu Lys Asn  
145 150 155 160

His His Tyr Val Glu Leu Leu Gly Met Ser Glu Asp Ala Arg Glu Glu  
165 170 175

Tyr Ile Tyr Gln Phe Phe Glu Asp Lys Arg Trp Ala Met Lys Val Phe  
180 185 190

Ser Ser Leu Lys Ser Asn Glu Met Leu Phe Ser Met Cys Gln Val Pro  
195 200 205

Leu Val Cys Trp Ala Ala Cys Thr Cys Leu Lys Gln Gln Met Glu Lys  
210 215 220

Gly Gly Asp Val Thr Leu Thr Cys Gln Thr Thr Thr Ala Leu Phe Thr  
225 230 235 240

Cys Tyr Ile Ser Ser Leu Phe Thr Pro Val Asp Gly Gly Ser Pro Ser  
245 250 255

Leu Pro Asn Gln Ala Gln Leu Arg Arg Leu Cys Gln Val Ala Ala Lys  
260 265 270

Gly Ile Trp Thr Met Thr Tyr Val Phe Tyr Arg Glu Asn Leu Arg Arg  
275 280 285

Leu Gly Leu Thr Gln Ser Asp Val Ser Ser Phe Met Asp Ser Asn Ile  
290 295 300

Ile Gln Lys Asp Ala Glu Tyr Glu Asn Cys Tyr Val Phe Thr His Leu  
305 310 315 320

His Val Gln Glu Phe Phe Ala Ala Met Phe Tyr Met Leu Lys Gly Ser  
325 330 335

Trp Glu Ala Gly Asn Pro Ser Cys Gln Pro Phe Glu Asp Leu Lys Ser  
340 345 350

Leu Leu Gln Ser Thr Ser Tyr Lys Asp Pro His Leu Thr Gln Met Lys  
355 360 365

Cys Phe Leu Phe Gly Leu Leu Asn Glu Asp Arg Val Lys Gln Leu Glu  
370 375 380

Arg Thr Phe Asn Cys Lys Met Ser Leu Lys Ile Lys Ser Lys Leu Leu  
385 390 395 400

Gln Cys Met Glu Val Leu Gly Asn Ser Asp Tyr Ser Pro Ser Gln Leu  
405 410 415

Gly Phe Leu Glu Leu Phe His Cys Leu Tyr Glu Thr Gln Asp Lys Ala  
420 425 430

Phe Ile Ser Gln Ala Met Arg Cys Phe Pro Lys Val Ala Ile Asn Ile  
435 440 445

Cys Glu Lys Ile His Leu Leu Val Ser Ser Phe Cys Leu Lys His Cys  
450 455 460

Arg Cys Leu Arg Thr Ile Arg Leu Ser Val  
465 470

<210> 168  
<211> 472  
<212> PRT  
<213> Homo sapiens

<400> 168

Leu Asp Arg Leu Phe Ala Pro Lys Glu Thr Gly Lys Gln Pro Arg Thr  
1 5 10 15

Val Ile Ile Gln Gly Pro Gln Gly Ile Gly Lys Thr Thr Leu Leu Met  
20 25 30

Lys Leu Met Met Ala Trp Ser Asp Asn Lys Ile Phe Arg Asp Arg Phe  
35 40 45

Leu Tyr Thr Phe Tyr Phe Cys Cys Arg Glu Leu Arg Glu Leu Pro Pro  
50 55 60

Thr Ser Leu Ala Asp Leu Ile Ser Arg Glu Trp Pro Asp Pro Ala Ala

65

70

75

80

Pro Ile Thr Glu Ile Val Ser Gln Pro Glu Arg Leu Leu Phe Val Ile  
85 90 95

Asp Ser Phe Glu Glu Leu Gln Gly Gly Leu Asn Glu Pro Asp Ser Asp  
100 105 110

Leu Cys Gly Asp Leu Met Glu Lys Arg Pro Val Gln Val Leu Leu Ser  
115 120 125

Ser Leu Leu Arg Lys Lys Met Leu Pro Glu Ala Ser Leu Leu Ile Ala  
130 135 140

Ile	Lys	Pro	Val	Cys	Pro	Lys	Glu	Leu	Arg	Asp	Gln	Val	Thr	Ile	Ser
145					150					155					160

Glu Ile Tyr Gln Pro Arg Gly Phe Asn Glu Ser Asp Arg Leu Val Tyr  
165 170 175

Phe Cys Cys Phe Phe Lys Asp Pro Lys Arg Ala Met Glu Ala Phe Asn  
 180 185 190

Leu Val Arg Glu Ser Glu Gln Leu Phe Ser Ile Cys Gln Ile Pro Leu  
195 200 205

Leu Cys Trp Ile Leu Cys Thr Ser Leu Lys Gln Glu Met Gln Lys Gly  
210 215 220

Lys Asp Leu Ala Leu Thr Cys Gln Ser Thr Thr Ser Val Tyr Ser Ser  
225                    230                    235                    240

Phe Val Phe Asn Leu Phe Thr Pro Glu Gly Ala Glu Gly Pro Thr Pro  
245 250 255

Gln Thr Gln His Gln Leu Lys Ala Leu Cys Ser Leu Ala Ala Glu Gly  
260 265 270

Met Trp Thr Asp Thr Phe Glu Phe Cys Glu Asp Asp Leu Arg Arg Asn  
275 280 285

Gly Val Val Asp Ala Asp Ile Pro Ala Leu Leu Gly Thr Lys Ile Leu  
290 295 300

Leu Lys Tyr Gly Glu Arg Glu Ser Ser Tyr Val Phe Leu His Val Cys  
 305                    310                    315                    320

Ile Gln Glu Phe Cys Ala Ala Leu Phe Tyr Leu Leu Lys Ser His Leu  
325 330 335

Asp His Pro His Pro Ala Val Arg Cys Val Gln Glu Leu Leu Val Ala  
340 345 350

Asn Phe Glu Lys Ala Arg Arg Ala His Trp Ile Phe Leu Gly Cys Phe  
355 360 365

Leu Thr Gly Leu Leu Asn Lys Lys Glu Gln Glu Lys Leu Asp Ala Phe  
370 375 380

Phe Gly Phe Gln Leu Ser Gln Glu Ile Lys Gln Gln Ile His Gln Cys  
385 390 395 400

Leu Lys Ser Leu Gly Glu Arg Gly Asn Pro Gln Gly Gln Val Asp Ser  
405 410 415

Leu Ala Ile Phe Tyr Cys Leu Phe Glu Met Gln Asp Pro Ala Phe Val  
420 425 430

Lys Gln Ala Val Asn Leu Leu Gln Glu Ala Asn Phe His Ile Ile Asp  
435 440 445

Asn Val Asp Leu Val Val Ser Ala Tyr Cys Leu Lys Tyr Cys Ser Ser  
450 455 460

Leu Arg Lys Leu Cys Phe Ser Val  
465 470

<210> 169

<211> 477

<212> PRT

<213> Homo sapiens

<400> 169

Leu Gln Arg Leu Leu Asp Pro Asn Arg Thr Arg Ala Gln Ala Gln Thr  
1 5 10 15

Ile Val Leu Val Gly Arg Ala Gly Val Gly Lys Thr Thr Leu Ala Met  
20 25 30

Arg Ala Met Leu His Trp Ala Asn Gly Val Leu Phe Gln Gln Arg Phe  
35 40 45

Ser Tyr Val Phe Tyr Leu Ser Cys His Lys Ile Arg Tyr Met Lys Glu  
50 55 60

Thr Thr Phe Ala Glu Leu Ile Ser Leu Asp Trp Pro Asp Phe Asp Ala  
65 70 75 80

Pro Ile Glu Glu Phe Met Ser Gln Pro Glu Lys Leu Leu Phe Ile Ile  
85 90 95

Asp Gly Phe Glu Glu Ile Ile Ser Glu Ser Arg Ser Glu Ser Leu  
100 105 110

Asp Asp Gly Ser Pro Cys Thr Asp Trp Tyr Gln Glu Leu Pro Val Thr  
115 120 125

Lys Ile Leu His Ser Leu Leu Lys Lys Glu Leu Val Pro Leu Ala Thr  
130 135 140

Leu Leu Ile Thr Ile Lys Thr Trp Phe Val Arg Asp Leu Lys Ala Ser  
145 150 155 160

Leu Val Asn Pro Cys Phe Val Gln Ile Thr Gly Phe Thr Gly Asp Asp  
165 170 175

Leu Arg Val Tyr Phe Met Arg His Phe Asp Asp Ser Ser Glu Val Glu  
180 185 190

Lys Ile Leu Gln Gln Leu Arg Lys Asn Glu Thr Leu Phe His Ser Cys  
195 200 205

Ser Ala Pro Met Val Cys Trp Thr Val Cys Ser Cys Leu Lys Gln Pro  
210 215 220

Lys Val Arg Tyr Tyr Asp Leu Gln Ser Ile Thr Gln Thr Thr Thr Ser  
225 230 235 240

Leu Tyr Ala Tyr Phe Phe Ser Asn Leu Phe Ser Thr Ala Glu Val Asp  
245 250 255

Leu Ala Asp Asp Ser Trp Pro Gly Gln Trp Arg Ala Leu Cys Ser Leu  
260 265 270

Ala Ile Glu Gly Leu Trp Ser Met Asn Phe Thr Phe Asn Lys Glu Asp  
275 280 285

Thr Glu Ile Glu Gly Leu Glu Val Pro Phe Ile Asp Ser Leu Tyr Glu

290

295

300

Phe Asn Ile Leu Gln Lys Ile Asn Asp Cys Gly Gly Cys Thr Thr Phe  
305                   310                   315                   320

Thr His Leu Ser Phe Gln Glu Phe Phe Ala Ala Met Ser Phe Val Leu  
325                   330                   335

Glu Glu Pro Arg Glu Phe Pro Pro His Ser Thr Lys Pro Gln Glu Met  
340                   345                   350

Lys Met Leu Leu Gln His Val Leu Leu Asp Lys Glu Ala Tyr Trp Thr  
355                   360                   365

Pro Val Val Leu Phe Phe Phe Gly Leu Leu Asn Lys Asn Ile Ala Arg  
370                   375                   380

Glu Leu Glu Asp Thr Leu His Cys Lys Ile Ser Pro Arg Val Met Glu  
385                   390                   395                   400

Glu Leu Leu Lys Trp Gly Glu Glu Leu Gly Lys Ala Glu Ser Ala Ser  
405                   410                   415

Leu Gln Phe His Ile Leu Arg Leu Phe His Cys Leu His Glu Ser Gln  
420                   425                   430

Glu Glu Asp Phe Thr Lys Lys Met Leu Gly Arg Ile Phe Glu Val Asp  
435                   440                   445

Leu Asn Ile Leu Glu Asp Glu Glu Leu Gln Ala Ser Ser Phe Cys Leu  
450                   455                   460

Lys His Cys Lys Arg Leu Asn Lys Leu Arg Leu Ser Val  
465                   470                   475

<210> 170

<211> 473

<212> PRT

<213> Homo sapiens

<400> 170

Leu Pro Cys Leu Leu Pro Lys Arg Pro Gln Gly Arg Gln Pro Lys  
1                   5                   10                   15

Thr Val Ala Ile Gln Gly Ala Pro Gly Ile Gly Lys Thr Ile Leu Ala  
20                   25                   30

Lys Lys Val Met Phe Glu Trp Ala Arg Asn Lys Phe Tyr Ala His Lys  
35 40 45

Arg Trp Cys Ala Phe Tyr Phe His Cys Gln Glu Val Asn Gln Thr Thr  
50 55 60

Asp Gln Ser Phe Ser Glu Leu Ile Glu Gln Lys Trp Pro Gly Ser Gln  
65 70 75 80

Asp Leu Val Ser Lys Ile Met Ser Lys Pro Asp Gln Leu Leu Leu Leu  
85 90 95

Leu Asp Gly Phe Glu Glu Leu Thr Ser Thr Leu Ile Asp Arg Leu Glu  
100 105 110

Asp Leu Ser Glu Asp Trp Arg Gln Lys Leu Pro Gly Ser Val Leu Leu  
115 120 125

Ser Ser Leu Leu Ser Lys Thr Met Leu Pro Glu Ala Thr Leu Leu Ile  
130 135 140

Met Ile Arg Phe Thr Ser Trp Gln Thr Cys Lys Pro Leu Leu Lys Cys  
145 150 155 160

Pro Ser Leu Val Thr Leu Pro Gly Phe Asn Thr Met Glu Lys Ile Lys  
165 170 175

Tyr Phe Gln Met Tyr Phe Gly His Thr Glu Glu Gly Asp Gln Val Leu  
180 185 190

Ser Phe Ala Met Glu Asn Thr Ile Leu Phe Ser Met Cys Arg Val Pro  
195 200 205

Val Val Cys Trp Met Val Cys Ser Gly Leu Lys Gln Gln Met Glu Arg  
210 215 220

Gly Asn Asn Leu Thr Gln Ser Cys Pro Asn Ala Thr Ser Val Phe Val  
225 230 235 240

Arg Tyr Ile Ser Ser Leu Phe Pro Thr Arg Ala Glu Asn Phe Ser Arg  
245 250 255

Lys Ile His Gln Ala Gln Leu Glu Gly Leu Cys His Leu Ala Ala Asp  
260 265 270

Ser Met Trp His Arg Lys Trp Val Leu Gly Lys Glu Asp Leu Glu Glu  
275 280 285

Ala Lys Leu Asp Gln Thr Gly Val Thr Ala Phe Leu Gly Met Ser Ile  
290 295 300

Leu Arg Arg Ile Ala Gly Glu Glu Asp His Tyr Val Phe Thr Leu Val  
305 310 315 320

Thr Phe Gln Glu Phe Phe Ala Ala Leu Phe Tyr Val Leu Cys Phe Pro  
325 330 335

Gln Arg Leu Lys Asn Phe His Val Leu Ser His Val Asn Ile Gln Arg  
340 345 350

Leu Ile Ala Ser Pro Arg Gly Ser Lys Ser Tyr Leu Ser His Met Gly  
355 360 365

Leu Phe Leu Phe Gly Phe Leu Asn Glu Ala Cys Ala Ser Ala Val Glu  
370 375 380

Gln Ser Phe Gln Cys Lys Val Ser Phe Gly Asn Lys Arg Lys Leu Leu  
385 390 395 400

Lys Val Ile Pro Leu Leu His Lys Cys Asp Pro Pro Ser Pro Gly Ser  
405 410 415

Gly Val Pro Gln Leu Phe Tyr Cys Leu His Glu Ile Arg Glu Glu Ala  
420 425 430

Phe Val Ser Gln Ala Leu Asn Asp Tyr His Lys Val Val Leu Arg Ile  
435 440 445

Gly Asn Asn Lys Glu Val Gln Val Ser Ala Phe Cys Leu Lys Arg Cys  
450 455 460

Gln Tyr Leu His Glu Val Glu Leu Thr  
465 470

<210> 171  
<211> 470  
<212> PRT  
<213> Homo sapiens

<400> 171

Val Glu Ala Leu Phe Asp Ser Gly Glu Lys Pro Ser Leu Ala Pro Ser  
1 5 10 15

Leu Val Val Leu Gln Gly Ser Ala Gly Thr Gly Lys Thr Thr Leu Ala  
20 25 30

Arg Lys Met Val Leu Asp Trp Ala Thr Gly Thr Leu Tyr Pro Gly Arg  
35 40 45

Phe Asp Tyr Val Phe Tyr Val Ser Cys Lys Glu Val Val Leu Leu Leu  
50 55 60

Glu Ser Lys Leu Glu Gln Leu Leu Phe Trp Cys Cys Gly Asp Asn Gln  
65 70 75 80

Ala Pro Val Thr Glu Ile Leu Arg Gln Pro Glu Arg Leu Leu Phe Ile  
85 90 95

Leu Asp Gly Phe Asp Glu Leu Gln Arg Pro Phe Glu Glu Lys Leu Lys  
100 105 110

Lys Arg Gly Leu Ser Pro Lys Glu Ser Leu Leu His Leu Leu Ile Arg  
115 120 125

Arg His Thr Leu Pro Thr Cys Ser Leu Leu Ile Thr Thr Arg Pro Leu  
130 135 140

Ala Leu Arg Asn Leu Glu Pro Leu Leu Lys Gln Ala Arg His Val His  
145 150 155 160

Ile Leu Gly Phe Ser Glu Glu Arg Ala Arg Tyr Phe Ser Ser Tyr  
165 170 175

Phe Thr Asp Glu Lys Gln Ala Asp Arg Ala Phe Asp Ile Val Gln Lys  
180 185 190

Asn Asp Ile Leu Tyr Lys Ala Cys Gln Val Pro Gly Ile Cys Trp Val  
195 200 205

Val Cys Ser Trp Leu Gln Gly Gln Met Glu Arg Gly Lys Val Val Leu  
210 215 220

Glu Thr Pro Arg Asn Ser Thr Asp Ile Phe Met Ala Tyr Val Ser Thr  
225 230 235 240

Phe Leu Pro Pro Asp Asp Asp Gly Gly Cys Ser Glu Leu Ser Arg His  
245 250 255

Arg Val Leu Arg Ser Leu Cys Ser Leu Ala Ala Glu Gly Ile Gln His  
260 265 270

Gln Arg Phe Leu Phe Glu Glu Ala Glu Leu Arg Lys His Asn Leu Asp  
275 280 285

Gly Pro Arg Leu Ala Ala Phe Leu Ser Ser Asn Asp Tyr Gln Leu Gly  
290 295 300

Leu Ala Ile Lys Lys Phe Tyr Ser Phe Arg His Ile Ser Phe Gln Asp  
305 310 315 320

Phe Phe His Ala Met Ser Tyr Leu Val Lys Glu Asp Gln Ser Arg Leu  
325 330 335

Gly Lys Glu Ser Arg Arg Glu Val Gln Arg Leu Leu Glu Val Lys Glu  
340 345 350

Gln Glu Gly Asn Asp Glu Met Thr Leu Thr Met Gln Phe Leu Leu Asp  
355 360 365

Ile Ser Lys Lys Asp Ser Phe Ser Asn Leu Glu Leu Lys Phe Cys Phe  
370 375 380

Arg Ile Ser Pro Cys Leu Ala Gln Asp Leu Lys His Phe Lys Glu Gln  
385 390 395 400

Met Glu Ser Met Lys His Asn Arg Thr Trp Asp Leu Glu Phe Ser Leu  
405 410 415

Tyr Glu Ala Lys Ile Lys Asn Leu Val Lys Gly Ile Gln Met Asn Asn  
420 425 430

Val Ser Phe Lys Ile Lys His Ser Asn Glu Lys Lys Ser Gln Ser Gln  
435 440 445

Asn Leu Phe Ser Val Lys Ser Ser Leu Ser His Gly Pro Lys Glu Glu  
450 455 460

Gln Lys Cys Pro Ser Val  
465 470

<210> 172  
<211> 466  
<212> PRT  
<213> Homo sapiens

<400> 172

Leu Ile Pro Phe Ser Asn Pro Arg Val Leu Pro Gly Pro Phe Ser Tyr  
1 5 10 15

Thr Val Val Leu Tyr Gly Pro Ala Gly Leu Gly Lys Thr Thr Leu Ala  
20 25 30

Gln Lys Leu Met Leu Asp Trp Ala Glu Asp Asn Leu Ile His Lys Phe  
35 40 45

Lys Tyr Ala Phe Tyr Leu Ser Cys Arg Glu Leu Ser Arg Leu Gly Pro  
50 55 60

Cys Ser Phe Ala Glu Leu Val Phe Arg Asp Trp Pro Glu Leu Gln Asp  
65 70 75 80

Asp Ile Pro His Ile Leu Ala Gln Ala Arg Lys Ile Leu Phe Val Ile  
85 90 95

Asp Gly Phe Asp Glu Leu Gly Ala Ala Pro Gly Ala Leu Ile Glu Asp  
100 105 110

Ile Cys Gly Asp Trp Glu Lys Lys Pro Val Pro Val Leu Leu Gly  
115 120 125

Ser Leu Leu Asn Arg Val Met Leu Pro Lys Ala Ala Leu Leu Val Thr  
130 135 140

Thr Arg Pro Arg Ala Leu Arg Asp Leu Arg Ile Leu Ala Glu Glu Pro  
145 150 155 160

Ile Tyr Ile Arg Val Glu Gly Phe Leu Glu Asp Arg Arg Ala Tyr  
165 170 175

Phe Leu Arg His Phe Gly Asp Glu Asp Gln Ala Met Arg Ala Phe Glu  
180 185 190

Leu Met Arg Ser Asn Ala Ala Leu Phe Gln Leu Gly Ser Ala Pro Ala  
195 200 205

Val Cys Trp Ile Val Cys Thr Thr Leu Lys Leu Gln Met Glu Lys Gly  
210 215 220

Glu Asp Pro Val Pro Thr Cys Leu Thr Arg Thr Gly Leu Phe Leu Arg  
225 230 235 240

Phe Leu Cys Ser Arg Phe Pro Gln Gly Ala Gln Leu Arg Gly Ala Leu  
245 250 255

Arg Thr Leu Ser Leu Leu Ala Ala Gln Gly Leu Trp Ala Gln Thr Ser  
260 265 270

Val Leu His Arg Glu Asp Leu Glu Arg Leu Gly Val Gln Glu Ser Asp  
275 280 285

Leu Arg Leu Phe Leu Asp Gly Asp Ile Leu Arg Gln Asp Arg Val Ser  
290 295 300

Lys Gly Cys Tyr Ser Phe Ile His Leu Ser Phe Gln Gln Phe Leu Thr  
305 310 315 320

Ala Leu Phe Tyr Thr Leu Glu Lys Glu Glu Glu Asp Arg Asp Gly  
325 330 335

His Thr Trp Asp Ile Gly Asp Val Gln Lys Leu Leu Ser Gly Val Glu  
340 345 350

Arg Leu Arg Asn Pro Asp Leu Ile Gln Ala Gly Tyr Tyr Ser Phe Gly  
355 360 365

Leu Ala Asn Glu Lys Arg Ala Lys Glu Leu Glu Ala Thr Phe Gly Cys  
370 375 380

Arg Met Ser Pro Asp Ile Lys Gln Glu Leu Leu Arg Cys Asp Ile Ser  
385 390 395 400

Cys Lys Gly Gly His Ser Thr Val Thr Asp Leu Gln Glu Leu Leu Gly  
405 410 415

Cys Leu Tyr Glu Ser Gln Glu Glu Leu Val Lys Glu Val Met Ala  
420 425 430

Gln Phe Lys Glu Ile Ser Leu His Leu Asn Ala Val Asp Val Val Pro  
435 440 445

Ser Ser Phe Cys Val Lys His Cys Arg Asn Leu Gln Lys Met Ser Leu  
450 455 460

Gln Val  
465

<210> 173  
<211> 476  
<212> PRT  
<213> Homo sapiens

<400> 173

Thr Leu Ala Gly Ala Phe Asp Ser Asp Arg Trp Gly Phe Arg Pro Arg  
1 5 10 15

Thr Val Val Leu His Gly Lys Ser Gly Ile Gly Lys Ser Ala Leu Ala  
20 25 30

Arg Arg Ile Val Leu Cys Trp Ala Gln Gly Gly Leu Tyr Gln Gly Met  
35 40 45

Phe Ser Tyr Val Phe Phe Leu Pro Val Arg Glu Met Gln Arg Lys Lys  
50 55 60

Glu Ser Ser Val Thr Glu Phe Ile Ser Arg Glu Trp Pro Asp Ser Gln  
65 70 75 80

Ala Pro Val Thr Glu Ile Met Ser Arg Pro Glu Arg Leu Leu Phe Ile  
85 90 95

Ile Asp Gly Phe Asp Asp Leu Gly Ser Val Leu Asn Asn Asp Thr Lys  
100 105 110

Leu Cys Lys Asp Trp Ala Glu Lys Gln Pro Pro Phe Thr Leu Ile Arg  
115 120 125

Ser Leu Leu Arg Lys Val Leu Leu Pro Glu Ser Phe Leu Ile Val Thr  
130 135 140

Val Arg Asp Val Gly Thr Glu Lys Leu Lys Ser Glu Val Val Ser Pro  
145 150 155 160

Arg Tyr Leu Leu Val Arg Gly Ile Ser Gly Glu Gln Arg Ile His Leu  
165 170 175

Leu Leu Glu Arg Gly Ile Gly Glu His Gln Lys Thr Gln Gly Leu Arg  
180 185 190

Ala Ile Met Asn Asn Arg Glu Leu Leu Asp Gln Cys Gln Val Pro Ala  
195 200 205

Val Gly Ser Leu Ile Cys Val Ala Leu Gln Leu Gln Asp Val Val Gly

210

215

220

Glu Ser Val Ala Pro Phe Asn Gln Thr Leu Thr Gly Leu His Ala Ala  
225                   230                   235                   240

Phe Val Phe His Gln Leu Thr Pro Arg Gly Val Val Arg Arg Cys Leu  
245                   250                   255

Asn Leu Glu Glu Arg Val Val Leu Lys Arg Phe Cys Arg Met Ala Val  
260                   265                   270

Glu Gly Val Trp Asn Arg Lys Ser Val Phe Asp Gly Asp Asp Leu Met  
275                   280                   285

Val Gln Gly Leu Gly Glu Ser Glu Leu Arg Ala Leu Phe His Met Asn  
290                   295                   300

Ile Leu Leu Pro Asp Ser His Cys Glu Glu Tyr Tyr Thr Phe Phe His  
305                   310                   315                   320

Leu Ser Leu Gln Asp Phe Cys Ala Ala Leu Tyr Tyr Val Leu Glu Gly  
325                   330                   335

Leu Glu Ile Glu Pro Ala Leu Cys Pro Leu Tyr Val Glu Lys Thr Lys  
340                   345                   350

Arg Ser Met Glu Leu Lys Gln Ala Gly Phe His Ile His Ser Leu Trp  
355                   360                   365

Met Lys Arg Phe Leu Phe Gly Leu Val Ser Glu Asp Val Arg Arg Pro  
370                   375                   380

Leu Glu Val Leu Leu Gly Cys Pro Val Pro Leu Gly Val Lys Gln Lys  
385                   390                   395                   400

Leu Leu His Trp Val Ser Leu Leu Gly Gln Gln Pro Asn Ala Thr Thr  
405                   410                   415

Pro Gly Asp Thr Leu Asp Ala Phe His Cys Leu Phe Glu Thr Gln Asp  
420                   425                   430

Lys Glu Phe Val Arg Leu Ala Leu Asn Ser Phe Gln Glu Val Trp Leu  
435                   440                   445

Pro Ile Asn Gln Asn Leu Asp Leu Ile Ala Ser Ser Phe Cys Leu Gln  
450                   455                   460

His Cys Pro Tyr Leu Arg Lys Ile Arg Val Asp Val  
465                    470                    475

<210> 174  
<211> 496  
<212> PRT  
<213> Homo sapiens

<400> 174

Thr Phe Asn Arg Leu Phe Arg Arg Asp Glu Glu Gly Arg Arg Pro Leu  
1                    5                    10                    15

Thr Val Val Leu Gln Gly Pro Ala Gly Ile Gly Lys Thr Met Ala Ala  
20                    25                    30

Lys Lys Ile Leu Tyr Asp Trp Ala Ala Gly Lys Leu Tyr Gln Gly Gln  
35                    40                    45

Val Asp Phe Ala Phe Phe Met Pro Cys Gly Glu Leu Leu Glu Arg Pro  
50                    55                    60

Gly Thr Arg Ser Leu Ala Asp Leu Ile Leu Asp Gln Cys Pro Asp Arg  
65                    70                    75                    80

Gly Ala Pro Val Pro Gln Met Leu Ala Gln Pro Gln Arg Leu Leu Phe  
85                    90                    95

Ile Leu Asp Gly Ala Asp Glu Leu Pro Ala Leu Gly Gly Pro Glu Ala  
100                    105                    110

Ala Pro Cys Thr Asp Pro Phe Glu Ala Ala Ser Gly Ala Arg Val Leu  
115                    120                    125

Gly Gly Leu Leu Ser Lys Ala Leu Leu Pro Thr Ala Leu Leu Leu Val  
130                    135                    140

Thr Thr Arg Ala Ala Ala Pro Gly Arg Leu Gln Gly Arg Leu Cys Ser  
145                    150                    155                    160

Pro Gln Cys Ala Glu Val Arg Gly Phe Ser Asp Lys Asp Lys Lys Lys  
165                    170                    175

Tyr Phe Tyr Lys Phe Phe Arg Asp Glu Arg Arg Ala Glu Arg Ala Tyr  
180                    185                    190

Arg Phe Val Lys Glu Asn Glu Thr Leu Phe Ala Leu Cys Phe Val Pro  
195 200 205

Phe Val Cys Trp Ile Val Cys Thr Val Leu Arg Gln Gln Leu Glu Leu  
210 215 220

Gly Arg Asp Leu Ser Arg Thr Ser Lys Thr Thr Ser Val Tyr Leu  
225 230 235 240

Leu Phe Ile Thr Ser Val Leu Ser Ser Ala Pro Val Ala Asp Gly Pro  
245 250 255

Arg Leu Gln Gly Asp Leu Arg Asn Leu Cys Arg Leu Ala Arg Glu Gly  
260 265 270

Val Leu Gly Arg Arg Ala Gln Phe Ala Glu Lys Glu Leu Glu Gln Leu  
275 280 285

Glu Leu Arg Gly Ser Lys Val Gln Thr Leu Phe Leu Ser Lys Lys Glu  
290 295 300

Leu Pro Gly Val Leu Glu Thr Glu Val Thr Tyr Gln Phe Ile Asp Gln  
305 310 315 320

Ser Phe Gln Glu Phe Leu Ala Ala Leu Ser Tyr Leu Leu Glu Asp Gly  
325 330 335

Gly Val Pro Arg Thr Ala Ala Gly Val Gly Thr Leu Leu Arg Gly  
340 345 350

Asp Ala Gln Pro His Ser His Leu Val Leu Thr Thr Arg Phe Leu Phe  
355 360 365

Gly Leu Leu Ser Ala Glu Arg Met Arg Asp Ile Glu Arg His Phe Gly  
370 375 380

Cys Met Val Ser Glu Arg Val Lys Gln Glu Ala Leu Arg Trp Val Gln  
385 390 395 400

Gly Gln Gly Gln Gly Cys Pro Gly Val Ala Pro Glu Val Thr Glu Gly  
405 410 415

Ala Lys Gly Leu Glu Asp Thr Glu Glu Pro Glu Glu Glu Gly  
420 425 430

Glu Glu Pro Asn Tyr Pro Leu Glu Leu Leu Tyr Cys Leu Tyr Glu Thr

435

440

445

Gln Glu Asp Ala Phe Val Arg Gln Ala Leu Cys Arg Phe Pro Glu Leu  
450 455 460

Ala Leu Gln Arg Val Arg Phe Cys Arg Met Asp Val Ala Val Leu Ser  
465 470 475 480

Tyr Cys Val Arg Cys Cys Pro Ala Gly Gln Ala Leu Arg Leu Ile Ser  
485 490 495

<210> 175

<211> 467

<212> PRT

<213> Homo sapiens

<400> 175

Leu Gln Leu Ala Tyr Asp Ser Thr Ser Tyr Tyr Ser Ala Asn Asn Leu  
1 5 10 15

\* Asn Val Phe Leu Met Gly Glu Arg Ala Ser Gly Lys Thr Ile Val Ile  
20 25 30

Asn Leu Ala Val Leu Arg Trp Ile Lys Gly Glu Met Trp Gln Asn Met  
35 40 45

Ile Ser Tyr Val Val His Leu Thr Ser His Glu Ile Asn Gln Met Thr  
50 55 60

Asn Ser Ser Leu Ala Glu Leu Ile Ala Lys Asp Trp Pro Asp Gly Gln  
65 70 75 80

Ala Pro Ile Ala Asp Ile Leu Ser Asp Pro Lys Lys Leu Leu Phe Ile  
85 90 95

Leu Glu Asp Leu Asp Asn Ile Arg Phe Glu Leu Asn Val Asn Glu Ser  
100 105 110

Ala Leu Cys Ser Asn Ser Thr Gln Lys Val Pro Ile Pro Val Leu Leu  
115 120 125

Val Ser Leu Leu Lys Arg Lys Met Ala Pro Gly Cys Trp Phe Leu Ile  
130 135 140

Ser Ser Arg Pro Thr Arg Gly Asn Asn Val Lys Thr Phe Leu Lys Glu  
145 150 155 160

Val Asp Cys Cys Thr Thr Leu Gln Leu Ser Asn Gly Lys Arg Glu Ile  
165 170 175

Tyr Phe Asn Ser Phe Phe Lys Asp Arg Gln Arg Ala Ser Ala Ala Leu  
180 185 190

Gln Leu Val His Glu Asp Glu Ile Leu Val Gly Leu Cys Arg Val Ala  
195 200 205

Ile Leu Cys Trp Ile Thr Cys Thr Val Leu Lys Arg Gln Met Asp Lys  
210 215 220

Gly Arg Asp Phe Gln Leu Cys Cys Gln Thr Pro Thr Asp Leu His Ala  
225 230 235 240

His Phe Leu Ala Asp Ala Leu Thr Ser Glu Ala Gly Leu Thr Ala Asn  
245 250 255

Gln Tyr His Leu Gly Leu Leu Lys Arg Leu Cys Leu Leu Ala Ala Gly  
260 265 270

Gly Leu Phe Leu Ser Thr Leu Asn Phe Ser Gly Glu Asp Leu Arg Cys  
275 280 285

Val Gly Phe Thr Glu Ala Asp Val Ser Val Leu Gln Ala Ala Asn Ile  
290 295 300

Leu Leu Pro Ser Asn Thr His Lys Asp Arg Tyr Lys Phe Ile His Leu  
305 .. 310 315 320

Asn Val Gln Glu Phe Cys Thr Ala Ile Ala Phe Leu Met Ala Val Pro  
325 330 335

Asn Tyr Leu Ile Pro Ser Gly Ser Arg Glu Tyr Lys Glu Lys Arg Glu  
340 345 350

Gln Tyr Ser Asp Phe Asn Gln Val Phe Thr Phe Ile Phe Gly Leu Leu  
355 360 365

Asn Ala Asn Arg Arg Lys Ile Leu Glu Thr Ser Phe Gly Tyr Gln Leu  
370 375 380

Pro Met Val Asp Ser Phe Lys Trp Tyr Ser Val Gly Tyr Met Lys His  
385 390 395 400

Leu Asp Arg Asp Pro Glu Lys Leu Thr His His Met Pro Leu Phe Tyr  
405 410 415

Cys Leu Tyr Glu Asn Arg Glu Glu Glu Phe Val Lys Thr Ile Val Asp  
420 425 430

Ala Leu Met Glu Val Thr Val Tyr Leu Gln Ser Asp Lys Asp Met Met  
435 440 445

Val Ser Leu Tyr Cys Leu Asp Tyr Cys Cys His Leu Arg Thr Leu Lys  
450 455 460

Leu Ser Val  
465

<210> 176  
<211> 454  
<212> PRT  
<213> Homo sapiens

<220>  
<221> MISC\_FEATURE  
<222> (178)..(178)  
<223> "Xaa" denotes any amino acid residue.

<220>  
<221> MISC\_FEATURE  
<222> (347)..(347)  
<223> "Xaa" denotes any amino acid residue.

<400> 176

Val Val Leu Gln Ala Cys Ala Gly Thr Gly Lys Thr Ala Val Val His  
1 5 10 15

Lys Phe Met Phe Asp Trp Ala Ala Gly Thr Val Thr Pro Gly Arg Cys  
20 25 30

Asp Tyr Leu Ile Tyr Val Asn Cys Ile Glu Ile Ser His Ile Ala Asn  
35 40 45

Leu Ser Ser Ala Asp Leu Ile Leu Thr Leu Phe Lys Ile Asn Gly Pro  
50 55 60

Ile Leu Asp Thr Ile Leu Ile Tyr Pro Lys Ile Leu Leu Ile Leu Asp  
65 70 75 80

Arg Phe Pro Glu Leu Gln Asp Pro Val Gly Asp Gln Glu Glu Asp Leu  
85 90 95

Ser Val His Pro Gln Glu Arg Arg Pro Val Glu Ser Leu Leu Cys Ser  
100 105 110

Phe Val Arg Lys Lys Leu Phe Pro Glu Ser Ser Leu Leu Ile Thr Ala  
115 120 125

Arg Pro Thr Ala Met Lys Lys Leu His Ser Leu Leu Lys Gln Pro Ile  
130 135 140

Gln Ala Glu Ile Leu Trp Phe Thr Asp Thr Glu Lys Arg Ala Tyr Leu  
145 150 155 160

Leu Ser Gln Phe Ser Gly Ala Asn Thr Thr Met Lys Val Phe Tyr Asp  
165 170 175

Leu Xaa Glu Asn Glu Asp Leu Asp Ile Met Ser Ser Leu Pro Ile Val  
180 185 190

Ser Trp Met Ile Cys Asn Val Leu Gln Ser Gln Gly Asp Gly Asp Arg  
195 200 205

Thr Leu Leu Arg Ser Leu Gln Thr Met Thr Asp Val Tyr Leu Phe Tyr  
210 215 220

Phe Ser Lys Cys Leu Lys Thr Leu Thr Gly Ile Ser Val Trp Glu Gly  
225 230 235 240

Gln Ser Cys Leu Trp Gly Leu Cys Arg Leu Ala Ala Glu Gly Leu Gln  
245 250 255

Asn His Gln Val Leu Phe Ala Val Ser Asp Leu Arg Arg His Gly Ile  
260 265 270

Gly Val Cys Asp Thr Asn Cys Thr Phe Leu Ser Arg Phe Leu Lys Lys  
275 280 285

Ala Glu Gly Ala Val Ser Val Tyr Thr Phe Leu His Phe Ser Phe Gln  
290 295 300

Glu Phe Leu Thr Ala Val Phe His Ala Leu Lys Asn Asp Asn Ser Trp  
305 310 315 320

Met Phe Phe Tyr Gln Ala Glu Lys Met Trp Gln Glu Met Phe Gln Gln  
325 330 335

Tyr Gly Lys Gly Phe Ser Ser Leu Met Ile Xaa Phe Leu Phe Gly Leu  
340 345 350

Leu His Lys Gly Lys Gly Ala Val Glu Thr Thr Phe Gly Arg Lys  
355 360 365

Val Ser Pro Gly Leu Gln Glu Glu Leu Leu Lys Trp Thr Glu Arg Glu  
370 375 380

Ile Lys Asp Lys Ser Ser Arg Leu Gln Ile Glu Pro Val Asp Leu Phe  
385 390 395 400

His Cys Leu Tyr Glu Ile Gln Glu Glu Tyr Ala Lys Arg Ile Ile  
405 410 415

Asp Asp Leu Gln Ser Ile Ile Leu Leu Gln Pro Thr Tyr Thr Lys Met  
420 425 430

Asp Ile Leu Val Met Ser Phe Cys Val Lys Ser Ser His Ser His Leu  
435 440 445

Ser Val Ser Leu Lys Cys  
450

<210> 177  
<211> 588  
<212> PRT  
<213> Homo sapiens

<400> 177

Leu Ser Gln Leu Phe Asn Pro Asp Ala Cys Gly Arg Arg Val Gln Thr  
1 5 10 15

Val Val Leu Tyr Gly Thr Val Gly Thr Gly Lys Ser Thr Leu Val Arg  
20 25 30

Lys Met Val Leu Asp Trp Cys Tyr Gly Arg Leu Pro Ala Phe Glu Leu  
35 40 45

Leu Ile Pro Phe Ser Cys Glu Asp Leu Ser Ser Leu Gly Pro Ala Pro  
50 55 60

Ala Ser Leu Cys Gln Leu Val Ala Gln Arg Tyr Thr Pro Leu Lys Glu  
65 70 75 80

Val Leu Pro Leu Met Ala Ala Gly Ser His Leu Leu Phe Val Leu  
85 90 95

His Gly Leu Glu His Leu Asn Leu Asp Phe Arg Leu Ala Gly Thr Gly  
100 105 110

Leu Cys Ser Asp Pro Glu Glu Pro Gln Glu Pro Ala Ala Ile Ile Val  
115 120 125

Asn Leu Leu Arg Lys Tyr Met Leu Pro Gln Ala Ser Ile Leu Val Thr  
130 135 140

Thr Arg Pro Ser Ala Ile Gly Arg Ile Pro Ser Lys Tyr Val Gly Arg  
145 150 155 160

Tyr Gly Glu Ile Cys Gly Phe Ser Asp Thr Asn Leu Gln Lys Leu Tyr  
165 170 175

Phe Gln Leu Arg Leu Asn Gln Pro Tyr Cys Gly Tyr Ala Val Gly Gly  
180 185 190

Ser Gly Val Ser Ala Thr Pro Ala Gln Arg Asp His Leu Val Gln Met  
195 200 205

Leu Ser Arg Asn Leu Glu Gly His His Gln Ile Ala Ala Ala Cys Phe  
210 215 220

Leu Pro Ser Tyr Cys Trp Leu Val Cys Ala Thr Leu His Phe Leu His  
225 230 235 240

Ala Pro Thr Pro Ala Gly Gln Thr Leu Thr Ser Ile Tyr Thr Ser Phe  
245 250 255

Leu Arg Leu Asn Phe Ser Gly Glu Thr Leu Asp Ser Thr Asp Pro Ser  
260 265 270

Asn Leu Ser Leu Met Ala Tyr Ala Ala Arg Thr Met Gly Lys Leu Ala  
275 280 285

Tyr Glu Gly Val Ser Ser Arg Lys Thr Tyr Phe Ser Glu Glu Asp Val  
290 295 300

Cys Gly Cys Leu Glu Ala Gly Ile Arg Thr Glu Glu Glu Phe Gln Leu  
305 310 315 320

Leu His Ile Phe Arg Arg Asp Ala Leu Arg Phe Phe Leu Ala Pro Cys  
325 330 335

Val Glu Pro Gly Arg Ala Gly Thr Phe Val Phe Thr Val Pro Ala Met  
340 345 350

Gln Glu Tyr Leu Ala Ala Leu Tyr Ile Val Leu Gly Leu Arg Lys Thr  
355 360 365

Thr Leu Gln Lys Val Gly Lys Glu Val Ala Glu Leu Val Gly Arg Val  
370 375 380

Gly Glu Asp Val Ser Leu Val Leu Gly Ile Met Ala Lys Leu Leu Pro  
385 390 395 400

Leu Arg Ala Leu Pro Leu Leu Phe Asn Leu Ile Lys Val Val Pro Arg  
405 410 415

Val Phe Gly Arg Met Val Gly Lys Ser Arg Glu Ala Val Ala Gln Ala  
420 425 430

Met Val Leu Glu Met Phe Arg Glu Glu Asp Tyr Tyr Asn Asp Asp Val  
435 440 445

Leu Asp Gln Met Gly Ala Ser Ile Leu Gly Val Glu Gly Pro Arg Arg  
450 455 460

His Pro Asp Glu Pro Pro Glu Asp Glu Val Phe Glu Leu Phe Pro Met  
465 470 475 480

Phe Met Gly Gly Leu Leu Ser Ala His Asn Arg Ala Val Leu Ala Gln  
485 490 495

Leu Gly Cys Pro Ile Lys Asn Leu Asp Ala Leu Glu Asn Ala Gln Ala  
500 505 510

Ile Lys Lys Lys Leu Gly Lys Leu Gly Arg Gln Val Leu Pro Pro Ser  
515 520 525

Glu Leu Leu Asp His Leu Phe Phe His Tyr Glu Phe Gln Asn Gln Arg  
530 535 540

Phe Ser Ala Glu Val Leu Ser Ser Leu Arg Gln Leu Asn Leu Ala Gly  
545 550 555 560

Val Arg Met Thr Pro Val Lys Cys Thr Val Val Ala Ala Val Leu Gly  
565 570 575

Ser Gly Arg His Ala Leu Asp Glu Val Asn Leu Ala  
580                                   585

<210> 178  
<211> 467  
<212> PRT  
<213> Homo sapiens  
  
<400> 178

Glu Val Leu Leu Ala Ala Lys Glu His Arg Arg Pro Arg Glu Thr Arg  
1                                   5                                   10                           15

Val Ile Ala Val Leu Gly Lys Ala Gly Gln Gly Lys Ser Tyr Trp Ala  
20                                   25                                   30

Gly Ala Val Ser Arg Ala Trp Ala Cys Gly Arg Leu Pro Gln Tyr Asp  
35                                   40                                   45

Phe Val Phe Ser Val Pro Cys His Cys Leu Asn Arg Pro Gly Asp Ala  
50                                   55                                   60

Tyr Gly Leu Gln Asp Leu Leu Phe Ser Leu Gly Pro Gln Pro Leu Val  
65                                   70                                   75                           80

Ala Ala Asp Glu Val Phe Ser His Ile Leu Lys Arg Pro Asp Arg Val  
85                                   90                                   95

Leu Leu Ile Leu Asp Ala Phe Glu Glu Leu Glu Ala Gln Asp Gly Phe  
100                                   105                                   110

Leu His Ser Thr Cys Gly Pro Ala Pro Ala Glu Pro Cys Ser Leu Arg  
115                                   120                                   125

Gly Leu Leu Ala Gly Leu Phe Gln Lys Lys Leu Leu Arg Gly Cys Thr  
130                                   135                                   140

Leu Leu Leu Thr Ala Arg Pro Arg Gly Arg Leu Val Gln Ser Leu Ser  
145                                   150                                   155                           160

Lys Ala Asp Ala Leu Phe Glu Leu Ser Gly Phe Ser Met Glu Gln Ala  
165                                   170                                   175

Gln Ala Tyr Val Met Arg Tyr Phe Glu Ser Ser Gly Met Thr Glu His  
180                                   185                                   190

Gln Asp Arg Ala Leu Thr Leu Leu Arg Asp Arg Pro Leu Leu Leu Ser  
195                                   200                                   205

His Ser His Ser Pro Thr Leu Cys Arg Ala Val Cys Gln Leu Ser Glu  
210 215 220

Ala Leu Leu Glu Leu Gly Glu Asp Ala Lys Leu Pro Ser Thr Leu Thr  
225 230 235 240

Gly Leu Tyr Val Gly Leu Leu Gly Arg Ala Ala Leu Asp Ser Pro Pro  
245 250 255

Gly Ala Leu Ala Glu Leu Ala Lys Leu Ala Trp Glu Leu Gly Arg Arg  
260 265 270

His Gln Ser Thr Leu Gln Glu Asp Gln Phe Pro Ser Ala Asp Val Arg  
275 280 285

Thr Trp Ala Met Ala Lys Gly Leu Val Gln His Pro Pro Arg Ala Ala  
290 295 300

Glu Ser Glu Leu Ala Phe Pro Ser Phe Leu Leu Gln Cys Phe Leu Gly  
305 310 315 320

Ala Leu Trp Leu Ala Leu Ser Gly Glu Ile Lys Asp Lys Glu Leu Pro  
325 330 335

Gln Tyr Leu Ala Leu Thr Pro Arg Lys Lys Arg Pro Tyr Asp Asn Trp  
340 345 350

Leu Glu Gly Val Pro Arg Phe Leu Ala Gly Leu Ile Phe Gln Pro Pro  
355 360 365

Ala Arg Cys Leu Gly Ala Leu Leu Gly Pro Ser Ala Ala Ala Ser Val  
370 375 380

Asp Arg Lys Gln Lys Val Leu Ala Arg Tyr Leu Lys Arg Leu Gln Pro  
385 390 395 400

Gly Thr Leu Arg Ala Arg Gln Leu Leu Glu Leu Leu His Cys Ala His  
405 410 415

Glu Ala Glu Glu Ala Gly Ile Trp Gln His Val Val Gln Glu Leu Pro  
420 425 430

Gly Arg Leu Ser Phe Leu Gly Thr Arg Leu Thr Pro Pro Asp Ala His  
435 440 445

Val Leu Gly Lys Ala Leu Glu Ala Ala Gly Gln Asp Phe Ser Leu Asp  
450 455 460

Leu Arg Ser  
465

<210> 179  
<211> 465  
<212> PRT  
<213> Homo sapiens

<400> 179

Val Ser Ile Ser Asp Leu Phe Asn Thr Arg Val Asn Lys Gly Pro Arg  
1 5 10 15

Val Thr Val Leu Leu Gly Lys Ala Gly Met Gly Lys Thr Thr Leu Ala  
20 25 30

His Arg Leu Cys Gln Lys Trp Ala Glu Gly His Leu Asn Cys Phe Gln  
35 40 45

Ala Leu Phe Leu Phe Glu Phe Arg Gln Leu Asn Leu Ile Thr Arg Phe  
50 55 60

Leu Thr Pro Ser Glu Leu Leu Phe Asp Leu Tyr Leu Ser Pro Glu Ser  
65 70 75 80

Asp His Asp Thr Val Phe Gln Tyr Leu Glu Lys Asn Ala Asp Gln Val  
85 90 95

Leu Leu Ile Phe Asp Gly Leu Asp Glu Ala Leu Gln Pro Met Gly Pro  
100 105 110

Asp Gly Pro Gly Pro Val Leu Thr Leu Phe Ser His Leu Cys Asn Gly  
115 120 125

Thr Leu Leu Pro Gly Cys Arg Val Met Ala Thr Ser Arg Pro Gly Lys  
130 135 140

Leu Pro Ala Cys Leu Pro Ala Glu Ala Ala Met Val His Met Leu Gly  
145 150 155 160

Phe Asp Gly Pro Arg Val Glu Glu Tyr Val Asn His Phe Phe Ser Ala  
165 170 175

Gln Pro Ser Arg Glu Gly Ala Leu Val Glu Leu Gln Thr Asn Gly Arg

180

185

190

Leu Arg Ser Leu Cys Ala Val Pro Ala Leu Cys Gln Val Ala Cys Leu  
195 200 205

Cys Leu His His Leu Leu Pro Asp His Ala Pro Gly Gln Ser Val Ala  
210 215 220

Leu Leu Pro Asn Met Thr Gln Leu Tyr Met Gln Met Val Leu Ala Leu  
225 230 235 240

Ser Pro Pro Gly His Leu Pro Thr Ser Ser Leu Leu Asp Leu Gly Glu  
245 250 255

Val Ala Leu Arg Gly Leu Glu Thr Gly Lys Val Ile Phe Tyr Ala Lys  
260 265 270

Asp Ile Ala Pro Pro Leu Ile Ala Phe Gly Ala Thr His Ser Leu Leu  
275 280 285

Thr Ser Phe Cys Val Cys Thr Gly Pro Gly His Gln Gln Thr Gly Tyr  
290 295 300

Ala Phe Thr His Leu Ser Leu Gln Glu Phe Leu Ala Ala Leu His Leu  
305 310 315 320

Met Ala Ser Pro Lys Val Asn Lys Asp Thr Leu Thr Gln Tyr Val Thr  
325 330 335

Leu His Ser Arg Trp Val Gln Arg Thr Lys Ala Arg Leu Gly Leu Ser  
340 345 350

Asp His Leu Pro Thr Phe Leu Ala Gly Leu Ala Ser Cys Thr Cys Arg  
355 360 365

Pro Phe Leu Ser His Leu Ala Gln Gly Asn Glu Asp Cys Val Gly Ala  
370 375 380

Lys Gln Ala Ala Val Val Gln Val Leu Lys Lys Leu Ala Thr Arg Lys  
385 390 395 400

Leu Thr Gly Pro Lys Val Val Glu Leu Cys His Cys Val Asp Glu Thr  
405 410 415

Gln Glu Pro Glu Leu Ala Ser Leu Thr Ala Gln Ser Leu Pro Tyr Gln  
420 425 430

Leu Pro Phe His Asn Phe Pro Leu Thr Cys Thr Asp Leu Ala Thr Leu  
435 440 445

Thr Asn Ile Leu Glu His Arg Glu Ala Pro Ile His Leu Asp Phe Asp  
450 455 460

Gly  
465

<210> 180  
<211> 501  
<212> PRT  
<213> Homo sapiens  
  
<400> 180

Leu Asp Arg Leu Phe Leu Pro Leu Ser Arg Val Ser Val Pro Pro Arg  
1 5 10 15

Val Ser Ile Thr Ile Gly Val Ala Gly Met Gly Lys Thr Thr Leu Val  
20 25 30

Arg His Phe Val Arg Leu Trp Ala His Gly Gln Val Gly Lys Asp Phe  
35 40 45

Ser Leu Val Leu Pro Leu Thr Phe Arg Asp Leu Asn Thr His Glu Lys  
50 55 60

Leu Cys Ala Asp Arg Leu Ile Cys Ser Val Phe Pro His Val Gly Glu  
65 70 75 80

Pro Ser Leu Ala Val Ala Val Pro Ala Arg Ala Leu Leu Ile Leu Asp  
85 90 95

Gly Leu Asp Glu Cys Arg Thr Pro Leu Asp Phe Ser Asn Thr Val Ala  
100 105 110

Cys Thr Asp Pro Lys Lys Glu Ile Pro Val Asp His Leu Ile Thr Asn  
115 120 125

Ile Ile Arg Gly Asn Leu Phe Pro Glu Val Ser Ile Trp Ile Thr Ser  
130 135 140

Arg Pro Ser Ala Ser Gly Gln Ile Pro Gly Gly Leu Val Asp Arg Met  
145 150 155 160

Thr Glu Ile Arg Gly Phe Asn Glu Glu Glu Ile Lys Val Cys Leu Glu  
165 170 175

Gln Met Phe Pro Glu Asp Gln Ala Leu Leu Gly Trp Met Leu Ser Gln  
180 185 190

Val Gln Ala Asp Arg Ala Leu Tyr Leu Met Cys Thr Val Pro Ala Phe  
195 200 205

Cys Arg Leu Thr Gly Met Ala Leu Gly His Leu Trp Arg Ser Arg Thr  
210 215 220

Gly Pro Gln Asp Ala Glu Leu Trp Pro Pro Arg Thr Leu Cys Glu Leu  
225 230 235 240

Tyr Ser Trp Tyr Phe Arg Met Ala Leu Ser Gly Glu Gly Gln Glu Lys  
245 250 255

Gly Lys Ala Ser Pro Arg Ile Glu Gln Val Ala His Gly Gly Arg Lys  
260 265 270

Met Val Gly Thr Leu Gly Arg Leu Ala Phe His Gly Leu Leu Lys Lys  
275 280 285

Lys Tyr Val Phe Tyr Glu Gln Asp Met Lys Ala Phe Gly Val Asp Leu  
290 295 300

Ala Leu Leu Gln Gly Ala Pro Cys Ser Cys Phe Leu Gln Arg Glu Glu  
305 310 315 320

Thr Leu Ala Ser Ser Val Ala Tyr Cys Phe Thr His Leu Ser Leu Gln  
325 330 335

Glu Phe Val Ala Ala Ala Tyr Tyr Tyr Gly Ala Ser Arg Arg Ala Ile  
340 345 350

Phe Asp Leu Phe Thr Glu Ser Gly Val Ser Trp Pro Arg Leu Gly Phe  
355 360 365

Leu Thr His Phe Arg Ser Ala Ala Gln Arg Ala Met Gln Ala Glu Asp  
370 375 380

Gly Arg Leu Asp Val Phe Leu Arg Phe Leu Ser Gly Leu Leu Ser Pro  
385 390 395 400

Arg Val Asn Ala Leu Leu Ala Gly Ser Leu Leu Ala Gln Gly Glu His

405

410

415

Gln Ala Tyr Arg Thr Gln Val Ala Glu Leu Leu Gln Gly Cys Leu Arg  
420 425 430

Pro Asp Ala Ala Val Cys Ala Arg Ala Ile Asn Val Leu His Cys Leu  
435 440 445

His Glu Leu Gln His Thr Glu Leu Ala Arg Ser Val Glu Glu Ala Met  
450 455 460

Glu Ser Gly Ala Leu Ala Arg Leu Thr Gly Pro Ala His Arg Ala Ala  
465 470 475 480

Leu Ala Tyr Leu Leu Gln Val Ser Asp Ala Cys Ala Gln Glu Ala Asn  
485 490 495

Leu Ser Leu Ser Leu  
500

<210> 181  
<211> 522  
<212> PRT  
<213> Homo sapiens

<400> 181

Leu Glu Glu Leu Phe Ser Thr Pro Gly His Leu Asn Asp. Asp Ala Asp  
1 5 10 15

Thr Val Leu Val Val Gly Glu Ala Gly Ser Gly Lys Ser Thr Leu Leu  
20 25 30

Gln Arg Leu His Leu Leu Trp Ala Ala Gly Gln Asp Phe Gln Glu Phe  
35 40 45

Leu Phe Val Phe Pro Phe Ser Cys Arg Gln Leu Gln Cys Met Ala Lys  
50 55 60

Pro Leu Ser Val Arg Thr Leu Leu Phe Glu His Cys Cys Trp Pro Asp  
65 70 75 80

Val Gly Gln Glu Asp Ile Phe Gln Leu Leu Leu Asp His Pro Asp Arg  
85 90 95

Val Leu Leu Thr Phe Asp Gly Phe Asp Glu Phe Lys Phe Arg Phe Thr  
100 105 110

Asp Arg Glu Arg His Cys Ser Pro Thr Asp Pro Thr Ser Val Gln Thr  
115 120 125

Leu Leu Phe Asn Leu Leu Gln Gly Asn Leu Leu Lys Asn Ala Arg Lys  
130 135 140

Val Val Thr Ser Arg Pro Ala Ala Val Ser Ala Phe Leu Arg Lys Tyr  
145 150 155 160

Ile Arg Thr Glu Phe Asn Leu Lys Gly Phe Ser Glu Gln Gly Ile Glu  
165 170 175

Leu Tyr Leu Arg Lys Arg His His Glu Pro Gly Val Ala Asp Arg Leu  
180 185 190

Ile Arg Leu Leu Gln Glu Thr Ser Ala Leu His Gly Leu Cys His Leu  
195 200 205

Pro Val Phe Ser Trp Met Val Ser Lys Cys His Gln Glu Leu Leu Leu  
210 215 220

Gln Glu Gly Gly Ser Pro Lys Thr Thr Asp Met Tyr Leu Leu Ile  
225 230 235 240

Leu Gln His Phe Leu Leu His Ala Thr Pro Pro Asp Ser Ala Ser Gln  
245 250 255

Gly Leu Gly Pro Ser Leu Leu Arg Gly Arg Leu Pro Thr Leu Leu His  
260 265 270

Leu Gly Arg Leu Ala Leu Trp Gly Leu Gly Met Cys Cys Tyr Val Phe  
275 280 285

Ser Ala Gln Gln Leu Gln Ala Ala Gln Val Ser Pro Asp Asp Ile Ser  
290 295 300

Leu Gly Phe Leu Val Arg Ala Lys Gly Val Val Pro Gly Ser Thr Ala  
305 310 315 320

Pro Leu Glu Phe Leu His Ile Thr Phe Gln Cys Phe Phe Ala Ala Phe  
325 330 335

Tyr Leu Ala Leu Ser Ala Asp Val Pro Pro Ala Leu Leu Arg His Leu  
340 345 350

Phe Asn Cys Gly Arg Pro Gly Asn Ser Pro Met Ala Arg Leu Leu Pro  
355 360 365

Thr Met Cys Ile Gln Ala Ser Glu Gly Lys Asp Ser Ser Val Ala Ala  
370 375 380

Leu Leu Gln Lys Ala Glu Pro His Asn Leu Gln Ile Thr Ala Ala Phe  
385 390 395 400

Leu Ala Gly Leu Leu Ser Arg Glu His Trp Gly Leu Leu Ala Glu Cys  
405 410 415

Gln Thr Ser Glu Lys Ala Leu Leu Arg Arg Gln Ala Cys Ala Arg Trp  
420 425 430

Cys Leu Ala Arg Ser Leu Arg Lys His Phe His Ser Ile Pro Pro Ala  
435 440 445

Ala Pro Gly Glu Ala Lys Ser Val His Ala Met Pro Gly Phe Ile Trp  
450 455 460

Leu Ile Arg Ser Leu Tyr Glu Met Gln Glu Glu Arg Leu Ala Arg Lys  
465 470 475 480

Ala Ala Arg Gly Leu Asn Val Gly His Leu Lys Leu Thr Phe Cys Ser  
485 490 495

Val Gly Pro Thr Glu Cys Ala Ala Leu Ala Phe Val Leu Gln His Leu  
500 505 510

Arg Arg Pro Val Ala Leu Gln Leu Asp Tyr  
515 520

<210> 182  
<211> 532  
<212> PRT  
<213> Homo sapiens

<400> 182

Ala Cys Leu Leu Asp His Thr Thr Gly Ile Leu Asn Glu Gln Gly Glu  
1 5 10 15

Thr Ile Phe Ile Leu Gly Asp Ala Gly Val Gly Lys Ser Met Leu Leu  
20 25 30

Gln Arg Leu Gln Ser Leu Trp Ala Thr Gly Arg Leu Asp Ala Gly Val  
35 40 45

Lys Phe Phe Phe His Phe Arg Cys Arg Met Phe Ser Cys Phe Lys Glu  
50 55 60

Ser Asp Arg Leu Cys Leu Gln Asp Leu Leu Phe Lys His Tyr Cys Tyr  
65 70 75 80

Pro Glu Arg Asp Pro Glu Glu Val Phe Ala Phe Leu Leu Arg Phe Pro  
85 90 95

His Val Ala Leu Phe Thr Phe Asp Gly Leu Asp Glu Leu His Ser Asp  
100 105 110

Leu Asp Leu Ser Arg Val Pro Asp Ser Ser Cys Pro Trp Glu Pro Ala  
115 120 125

His Pro Leu Val Leu Leu Ala Asn Leu Leu Ser Gly Lys Leu Leu Lys  
130 135 140

Gly Ala Ser Lys Leu Leu Thr Ala Arg Thr Gly Ile Glu Val Pro Arg  
145 150 155 160

Gln Phe Leu Arg Lys Lys Val Leu Leu Arg Gly Phe Ser Pro Ser His  
165 170 175

Leu Arg Ala Tyr Ala Arg Arg Met Phe Pro Glu Arg Ala Leu Gln Asp  
180 185 190

Arg Leu Leu Ser Gln Leu Glu Ala Asn Pro Asn Leu Cys Ser Leu Cys  
195 200 205

Ser Val Pro Leu Phe Cys Trp Ile Ile Phe Arg Cys Phe Gln His Phe  
210 215 220

Arg Ala Ala Phe Glu Gly Ser Pro Gln Leu Pro Asp Cys Thr Met Thr  
225 230 235 240

Leu Thr Asp Val Phe Leu Leu Val Thr Glu Val His Leu Asn Arg Met  
245 250 255

Gln Pro Ser Ser Leu Val Gln Arg Asn Thr Arg Ser Pro Val Glu Thr  
260 265 270

Leu His Ala Gly Arg Asp Thr Leu Cys Ser Leu Gly Gln Val Ala His  
275 280 285

Arg Gly Met Glu Lys Ser Leu Phe Val Phe Thr Gln Glu Glu Val Gln  
290 295 300

Ala Ser Gly Leu Gln Glu Arg Asp Met Gln Leu Gly Phe Leu Arg Ala  
305 310 315 320

Leu Pro Glu Leu Gly Pro Gly Gly Asp Gln Gln Ser Tyr Glu Phe Phe  
325 330 335

His Leu Thr Leu Gln Ala Phe Phe Thr Ala Phe Phe Leu Val Leu Asp  
340 345 350

Asp Arg Val Gly Thr Gln Glu Leu Leu Arg Phe Phe Gln Glu Trp Met  
355 360 365

Pro Pro Ala Gly Ala Ala Thr Thr Ser Cys Tyr Pro Pro Phe Leu Pro  
370 375 380

Phe Gln Cys Leu Gln Gly Ser Gly Pro Ala Arg Glu Asp Leu Phe Lys  
385 390 395 400

Asn Lys Asp His Phe Gln Phe Thr Asn Leu Phe Leu Cys Gly Leu Leu  
405 410 415

Ser Lys Ala Lys Gln Lys Leu Leu Arg His Leu Val Pro Ala Ala Ala  
420 425 430

Leu Arg Arg Lys Arg Lys Ala Leu Trp Ala His Leu Phe Ser Ser Leu  
435 440 445

Arg Gly Tyr Leu Lys Ser Leu Pro Arg Val Gln Val Glu Ser Phe Asn  
450 455 460

Gln Val Gln Ala Met Pro Thr Phe Ile Trp Met Leu Arg Cys Ile Tyr  
465 470 475 480

Glu Thr Gln Ser Gln Lys Val Gly Gln Leu Ala Ala Arg Gly Ile Cys  
485 490 495

Ala Asn Tyr Leu Lys Leu Thr Tyr Cys Asn Ala Cys Ser Ala Asp Cys  
500 505 510

Ser Ala Leu Ser Phe Val Leu His His Phe Pro Lys Arg Leu Ala Leu  
515 520 525

Asp Leu Asp Asn  
530

<210> 183  
<211> 312  
<212> PRT  
<213> Homo sapiens

<400> 183

Arg Val Glu Gln Leu Thr Leu Asn Gly Leu Leu Gln Ala Leu Gln Ser  
1 5 10 15

Pro Cys Ile Ile Glu Gly Glu Ser Gly Lys Gly Lys Ser Thr Leu Leu  
20 25 30

Gln Arg Ile Ala Met Leu Trp Gly Ser Gly Lys Cys Lys Ala Leu Thr  
35 40 45

Lys Phe Lys Phe Val Phe Phe Leu Arg Leu Ser Arg Ala Gln Gly Gly  
50 55 60

Leu Phe Glu Thr Leu Cys Asp Gln Leu Leu Asp Ile Pro Gly Thr Ile  
65 70 75 80

Arg Lys Gln Thr Phe Met Ala Met Leu Leu Lys Leu Arg Gln Arg Val  
85 90 95

Leu Phe Leu Leu Asp Gly Tyr Asn Glu Phe Lys Pro Gln Asn Cys Pro  
100 105 110

Glu Ile Glu Ala Leu Ile Lys Glu Asn His Arg Phe Lys Asn Met Val  
115 120 125

Ile Val Thr Thr Thr Glu Cys Leu Arg His Ile Arg Gln Phe Gly  
130 135 140

Ala Leu Thr Ala Glu Val Gly Asp Met Thr Glu Asp Ser Ala Gln Ala  
145 150 155 160

Leu Ile Arg Glu Val Leu Ile Lys Glu Leu Ala Glu Gly Leu Leu Leu  
165 170 175

Gln Ile Gln Lys Ser Arg Cys Leu Arg Asn Leu Met Lys Thr Pro Leu  
180 185 190

Phe Val Val Ile Thr Cys Ala Ile Gln Met Gly Glu Ser Glu Phe His  
195 200 205

Ser His Thr Gln Thr Thr Leu Phe His Thr Phe Tyr Asp Leu Leu Ile  
210                            215                            220

Gln Lys Asn Lys His Lys His Lys Gly Val Ala Ala Ser Asp Phe Ile  
225                            230                            235                            240

Arg Ser Leu Asp His Cys Gly Asp Leu Ala Leu Glu Gly Val Phe Ser  
245                            250                            255

His Lys Phe Asp Phe Glu Leu Gln Asp Val Ser Ser Val Asn Glu Asp  
260                            265                            270

Val Leu Leu Thr Thr Gly Leu Leu Cys Lys Tyr Thr Ala Gln Arg Phe  
275                            280                            285

Lys Pro Lys Tyr Lys Phe Phe His Lys Ser Phe Gln Glu Tyr Thr Ala  
290                            295                            300

Gly Arg Arg Leu Ser Ser Leu Leu  
305                            310

<210> 184

<211> 312

<212> PRT

<213> Homo sapiens

<400> 184

Val Gln Glu Pro Leu Val Leu Pro Glu Val Phe Gly Asn Leu Asn Ser  
1                            5                            10                            15

Val Met Cys Val Glu Gly Glu Ala Gly Ser Gly Lys Thr Val Leu Leu  
20                            25                            30

Lys Lys Ile Ala Phe Leu Trp Ala Ser Gly Cys Cys Pro Leu Leu Asn  
35                            40                            45

Arg Phe Gln Leu Val Phe Tyr Leu Ser Leu Ser Ser Thr Arg Pro Asp  
50                            55                            60

Glu Gly Leu Ala Ser Ile Ile Cys Asp Gln Leu Leu Glu Lys Glu Gly  
65                            70                            75                            80

Ser Val Thr Glu Met Cys Met Arg Asn Ile Ile Gln Gln Leu Lys Asn  
85                            90                            95

Gln Val Leu Phe Leu Leu Asp Asp Tyr Lys Glu Ile Cys Ser Ile Pro  
100 105 110

Gln Val Ile Gly Lys Leu Ile Gln Lys Asn His Leu Ser Arg Thr Cys  
115 120 125

Leu Leu Ile Ala Val Arg Thr Asn Arg Ala Arg Asp Ile Arg Arg Tyr  
130 135 140

Leu Glu Thr Ile Leu Glu Ile Lys Ala Phe Pro Phe Tyr Asn Thr Val  
145 150 155 160

Cys Ile Leu Arg Lys Leu Phe Ser His Asn Met Thr Arg Leu Arg Lys  
165 170 175

Phe Met Val Tyr Phe Gly Lys Asn Gln Ser Leu Gln Lys Ile Gln Lys  
180 185 190

Thr Pro Leu Phe Val Ala Ala Ile Cys Ala His Trp Phe Gln Tyr Pro  
195 200 205

Phe Asp Pro Ser Phe Asp Asp Val Ala Val Phe Lys Ser Tyr Met Glu  
210 215 220

Arg Leu Ser Leu Arg Asn Lys Ala Thr Ala Glu Ile Leu Lys Ala Thr  
225 230 235 240

Val Ser Ser Cys Gly Glu Leu Ala Leu Lys Gly Phe Phe Ser Cys Cys  
245 250 255

Phe Glu Phe Asn Asp Asp Asp Leu Ala Glu Ala Gly Val Asp Glu Asp  
260 265 270

Glu Asp Leu Thr Met Cys Leu Met Ser Lys Phe Thr Ala Gln Arg Leu  
275 280 285

Arg Pro Phe Tyr Arg Phe Leu Ser Pro Ala Phe Gln Glu Phe Leu Ala  
290 295 300

Gly Met Arg Leu Ile Glu Leu Leu  
305 310

<210> 185  
<211> 5601  
<212> DNA  
<213> Homo sapiens

<400> 185	
atggaccccg ttggcctcca gctcgcaac aagaacctgt ggagctgtct tgtgaggctg	60
ctcaccaaag acccagaatg gctgaacgcc aagatgaagt tcttcctccc caacacggac	120
ctggattcca ggaacgagac cttggaccct gaacagagag tcatactgca actcaacaag	180
ctgcatgtcc agggttcggc cacctggcag tcttcattc attgcgtgtg catgcagctg	240
gaggtgcctc tggacctgga ggtgcttctg ctaagtactt ttgctatga tgatgggttc	300
accagccagc tgggagctga gggaaaaagc caacctaata ctcaagctcca ccatggcctg	360
aagcgccccac atcagagctg tgggtcctca ccccgccgga agcagtgcaa gaagcagcag	420
ctagagttgg ccaagaagta cctgcagctc ctgcggaccc ctgcccagca gcgcctacagg	480
agccaaatcc ctgggtcagg gcagccccac gccttcacc accgttatgt ccctcaatc	540
ctgcgccggg ccacagcatc ctttagacact ccggaggggg ccattatggg ggacgtcaag	600
gtgaaagatg gtgctgacgt gagcatctcg gacctctca acaccaggta taacaaggc	660
ccgagggtga ccgtgctttt gggaaaggct ggcattggca agaccacgct ggcccaccgg	720
ctctgccaga agtggcaga gggccatctg aactgttcc agggccctgtt cttttgaa	780
ttccgccagc tcaacttgat cacgagggttc ctgacaccgt ccgagctcct tttgatctg	840
tacctgagcc ctgaatcgga ccacgacact gtcttcaggta acctggagaa gaacgctgac	900
caagtccctgc tgatcttga tggcttagat gaggccctcc agcctatggg tcctgatggc	960
ccaggcccag tcctcacccct tttccat ctctgcaatg ggaccctcct gcctggctgc	1020
cgggtgatgg ctacccccc tccaggaaag ctgcctgcct gcctgcctgc agaggcagcc	1080
atggccaca tggggcatt tgatggcca cgggtgaaag aatatgtaa tcacttctc	1140
agcgccccagc catcgccggg gggggccctg gtggagttac agacaaatgg acgtctccga	1200
agcctgtgtg cggtgccccgc actgtgccaa gtcgcctgca tctgcctcca ccatctgctt	1260
cctgaccacg ccccaggcca gtctgtggcc ctccctccca acatgactca gctctatatg	1320
cagatgggtgc tgcctctcag ccccccggg cacttgccca cctcgccct actggacctg	1380
ggggaggtgg ccctgaggggg cctggagaca gggaaaggta tcttctatgc aaaagatatt	1440
gctccaccct tgatagcttt tggggccact cacagcctgc tgacttcctt ctgcgtctgc	1500
acaggccctg ggcaccagca gacaggctat gctttcaccc acctcagcct gcaggagttt	1560
cttgctgccc tgcacccatgat ggccagcccc aaggtgaaca aagacacact tacccagtat	1620
gttaccctcc attcccgctg ggtacagcgg accaaagcta gactggccct ctcagaccac	1680
ctccccaccc tccctggcggg cctggcatcc tgcacccctgca gccccttcct tagccaccc	1740
gcgcaggggca atgaggactg tgggggtgcc aaggcaggctg ctgttagtgca ggtgttgaag	1800

aagttggcca	cccgcaagct	cacagggcc	aagggtttag	agctgtgtca	ctgtgtggat	1860
gagacacagg	agcctgagct	ggccagtctc	accgcacaaa	gcctccccta	tcaactgccc	1920
ttccacaatt	tcccactgac	ctgcaccgac	ctggccaccc	tgaccaacat	cctagagcac	1980
agggagggcc	ccatccacct	ggattttgat	ggctgtcccc	tggagcccca	ctgcccctgag	2040
gctctggtag	gctgtggca	gatagagaat	ctcagctta	agagcaggaa	gtgtggggat	2100
gcctttgcag	aagccctctc	caggagctt	ccgacaatgg	ggaggctgca	gatgctgggg	2160
ttagcagggaa	gtaaaatcac	tgcccggagc	atcagccacc	tggtaaaagc	tttgcctctc	2220
tgtccacagc	tgaaagaagt	cagtttcgg	gacaaccagc	tcagtgacca	ggtggtgctg	2280
aacatttgtgg	agtttctccc	tcacctacca	cggctccgga	agcttgacct	gagcagcaac	2340
agcatctgcg	tgtcaaccct	actctgctt	gcaagggtgg	cagtcacgt	tcctaccgtc	2400
aggatgcttc	aggccaggga	gcggaccatc	atcttccttc	tttccccgcc	cacagagaca	2460
actgcagagc	tacaaagagc	tccagacct	caggaaagt	acggccagag	gaaaggggct	2520
cagagcagaa	gcttgacgct	caggctgcag	aagtgtcagc	tccaggtcca	cgatgcggag	2580
gccctcatag	ccctgctcca	ggaaggccct	cacctggagg	aagtggacct	ctcagggAAC	2640
cagctggaag	atgaaggctg	tcggctgatg	gcagaggctg	catcccagct	gcacatcgcc	2700
aggaagctgg	acctcagcga	caacgggctt	tctgtggccg	gggtgcatt	tgtgctgagg	2760
gccgtgagtg	cgtgctggac	cctggcagag	ctgcacatca	gcctgcagca	caaaactgtg	2820
atcttcatgt	ttgcccagga	gccagaggag	cagaaggggc	cccaggagag	ggctgcattt	2880
cttgacagcc	tcatgctcca	gatgccctct	gagctgcctc	tgagctccc	aaggatgagg	2940
ctgacacatt	gtggcctcca	agaaaagcac	ctagagcagc	tctgcaaggc	tctggagga	3000
agctgccacc	tccgtcacct	ccaccccgac	ttctcaggca	atgctctggg	ggatgaaggt	3060
gcagcccccgc	tggctcagct	gtcccccagg	ctgggagctc	tgcagtcctt	gaacctcagt	3120
gagaacggtt	tgtccctgga	tgccgtgtt	ggcttggttc	ggtgtttctc	cactctgcag	3180
tggctcttcc	gcttggacat	cagtttgaa	agccaacaca	tcctcctgag	aggggacaag	3240
acaaggcaggg	atatgtgggc	cactggatct	ttgcccagact	tcccagctgc	agccaagttc	3300
ttagggttcc	gtcagcgctg	catccccagg	agcctctgcc	tcagtgagtg	tcctctggag	3360
cccccaagcc	tcacccgcct	ctgtgccact	ctgaaggact	gcccgggacc	cctggaaactg	3420
caattgtcct	gtgagttcct	gagtgaccag	agcctggaga	ctctactgga	ctgcttacct	3480
caactccctc	agctgagcct	gctgcagctg	agccagacgg	gactgtcccc	gaaaagccccc	3540
ttcctgctgg	ccaacacctt	aagcctgtgt	ccacgggtta	aaaaggtgga	tctcaggtcc	3600
ctgcaccatg	caactttgca	cttcagatcc	aacgaggagg	aggaaggcgt	gtgctgtggc	3660

aggttcacag	gctgcagcct	cagccaggag	cacgttagt	caactctgctg	gttgctgagc	3720
aagtgtaaag	acctcagcca	ggtggatctc	ttagcaaacc	tgctggcgaa	cagcggactc	3780
agatgccttc	tggaatgtct	gcggcagggt	ccccatctccg	gttgcttga	tctgagtcac	3840
aacagcattt	ctcaggaaag	tgccctgtac	ctgctggaga	caactgcctc	ctgcccacgt	3900
gtccgggagg	cctcagtgaa	cctgggctct	gagcagagct	tccggattca	cttctccaga	3960
gaggaccagg	ctgggaagac	actcaggcta	agtgagtgca	gctccggcc	agagcacgtg	4020
tccaggctgg	ccaccggctt	gagcaagtcc	ctgcagctga	cggagctcac	gctgacccag	4080
tgctgcctgg	gccagaagca	gctggccatc	ctcctgagct	tggggggcg	acccgoaggg	4140
ctgttcaGCC	tcagggtgca	ggagccgtgg	gcggacagag	ccagggttct	ctccctgtta	4200
gaagtctgct	cccaggcctc	aggcagtgtc	actgaaatca	gcatctccga	gaccacagcag	4260
cagctotgtg	tccagctgga	atttcctcgc	caggaagaga	atccagaagc	tgtggcactc	4320
aggttggctc	actgtgacct	tggagccac	cacagccttc	ttgtcggca	gctgatggag	4380
acatgtgcca	ggctgcagca	gctcagctt	tctcaggtta	acctctgtga	ggacgatgat	4440
gccagttccc	tgctgctgca	gagcctcctg	ctgtccctct	ctgagctgaa	gacatttcgg	4500
ctgacccctca	gctgtgtgag	cacccaggc	ctcgcccacc	tggcatctgg	tctggccac	4560
tgccaccact	tggaggagct	ggacttgtct	aacaatcaat	ttgatgagga	gggcaccaag	4620
gcgctgatga	ggggcccttga	ggggaaatgg	atgctaaaga	ggctggacct	cagtcacctt	4680
ctgctgaaca	gctccacctt	ggccttgctt	actcacagac	taagccagat	gacctgcctg	4740
cagagcctca	gactgaacag	gaacagtatac	ggtgatgtcg	tttgctgcca	cctttctgag	4800
gctctcaggg	ctgccaccag	cctagaggag	ctggacttga	gccacaacca	gattggagac	4860
gctgggttcc	agcacttagc	taccatcctg	cctgggctgc	cagagctcag	gaagatagac	4920
ctctcaggg	atagcatcag	ctcagccggg	ggagtgcagt	tggcagagtc	tctcggttctt	4980
tgcaggcgcc	tggaggagtt	gatgcttggc	tgcaatgccc	tggggatcc	cacagccctg	5040
gggctggctc	aggagctgcc	ccagcacctg	agggtcctac	acctaccatt	cagccatctg	5100
ggcccgagg	ggggccctgag	cctggcccag	gccctggatg	gatccccca	tttgaaagag	5160
atcagcttgg	cggaaaacaa	cctggctgga	ggggtcctgc	gtttctgtat	ggagctcccg	5220
ctgctcagac	agatagacct	ggtttcctgt	aagattgaca	accagactgc	caagctccctc	5280
acctccagct	tcacgagctg	ccctgcctg	gaagtaatct	tgctgtcctg	aatctccctc	5340
ggggatgagg	cagctgccga	gctggcccag	gtgctgccga	agatggcccg	gctgaagaga	5400
gtggacctgg	agaagaatca	gatcacagct	ttggggccct	ggctcctggc	tgaaggactg	5460

gcccaggggt ctagcatcca agtcatccgc ctctggaata accccattcc ctgcgacatg 5520  
gcccagcacc tgaagagcca ggagcccagg ctggactttg cttttttga caaccagccc 5580  
caggcccctt ggggtacttg a 5601

<210> 186  
<211> 1866  
<212> PRT  
<213> Homo sapiens

<400> 186

Met Asp Pro Val Gly Leu Gln Leu Gly Asn Lys Asn Leu Trp Ser Cys  
1 5 10 15

Leu Val Arg Leu Leu Thr Lys Asp Pro Glu Trp Leu Asn Ala Lys Met  
20 25 30

Lys Phe Phe Leu Pro Asn Thr Asp Leu Asp Ser Arg Asn Glu Thr Leu  
35 40 45

Asp Pro Glu Gln Arg Val Ile Leu Gln Leu Asn Lys Leu His Val Gln  
50 55 60

Gly Ser Asp Thr Trp Gln Ser Phe Ile His Cys Val Cys Met Gln Leu  
65 70 75 80

Glu Val Pro Leu Asp Leu Glu Val Leu Leu Leu Ser Thr Phe Gly Tyr  
85 90 95

Asp Asp Gly Phe Thr Ser Gln Leu Gly Ala Glu Gly Lys Ser Gln Pro  
100 105 110

Glu Ser Gln Leu His His Gly Leu Lys Arg Pro His Gln Ser Cys Gly  
115 120 125

Ser Ser Pro Arg Arg Lys Gln Cys Lys Lys Gln Gln Leu Glu Leu Ala  
130 135 140

Lys Lys Tyr Leu Gln Leu Leu Arg Thr Ser Ala Gln Gln Arg Tyr Arg  
145 150 155 160

Ser Gln Ile Pro Gly Ser Gly Gln Pro His Ala Phe His Gln Val Tyr  
165 170 175

Val Pro Pro Ile Leu Arg Arg Ala Thr Ala Ser Leu Asp Thr Pro Glu  
180 185 190

Gly Ala Ile Met Gly Asp Val Lys Val Glu Asp Gly Ala Asp Val Ser  
195 200 205

Ile Ser Asp Leu Phe Asn Thr Arg Val Asn Lys Gly Pro Arg Val Thr  
210 215 220

Val Leu Leu Gly Lys Ala Gly Met Gly Lys Thr Thr Leu Ala His Arg  
225 230 235 240

Leu Cys Gln Lys Trp Ala Glu Gly His Leu Asn Cys Phe Gln Ala Leu  
245 250 255

Phe Leu Phe Glu Phe Arg Gln Leu Asn Leu Ile Thr Arg Phe Leu Thr  
260 265 270

Pro Ser Glu Leu Leu Phe Asp Leu Tyr Leu Ser Pro Glu Ser Asp His  
275 280 285

Asp Thr Val Phe Gln Tyr Leu Glu Lys Asn Ala Asp Gln Val Leu Leu  
290 295 300

Ile Phe Asp Gly Leu Asp Glu Ala Leu Gln Pro Met Gly Pro Asp Gly  
305 310 315 320

Pro Gly Pro Val Leu Thr Leu Phe Ser His Leu Cys Asn Gly Thr Leu  
325 330 335

Leu Pro Gly Cys Arg Val Met Ala Thr Ser Arg Pro Gly Lys Leu Pro  
340 345 350

Ala Cys Leu Pro Ala Glu Ala Ala Met Val His Met Leu Gly Phe Asp  
355 360 365

Gly Pro Arg Val Glu Glu Tyr Val Asn His Phe Phe Ser Ala Gln Pro  
370 375 380

Ser Arg Glu Gly Ala Leu Val Glu Leu Gln Thr Asn Gly Arg Leu Arg  
385 390 395 400

Ser Leu Cys Ala Val Pro Ala Leu Cys Gln Val Ala Cys Leu Cys Leu  
405 410 415

His His Leu Leu Pro Asp His Ala Pro Gly Gln Ser Val Ala Leu Leu  
420 425 430

Pro Asn Met Thr Gln Leu Tyr Met Gln Met Val Leu Ala Leu Ser Pro  
435 440 445

Pro Gly His Leu Pro Thr Ser Ser Leu Leu Asp Leu Gly Glu Val Ala  
450 455 460

Leu Arg Gly Leu Glu Thr Gly Lys Val Ile Phe Tyr Ala Lys Asp Ile  
465 470 475 480

Ala Pro Pro Leu Ile Ala Phe Gly Ala Thr His Ser Leu Leu Thr Ser  
485 490 495

Phe Cys Val Cys Thr Gly Pro Gly His Gln Gln Thr Gly Tyr Ala Phe  
500 505 510

Thr His Leu Ser Leu Gln Glu Phe Leu Ala Ala Leu His Leu Met Ala  
515 520 525

Ser Pro Lys Val Asn Lys Asp Thr Leu Thr Gln Tyr Val Thr Leu His  
530 535 540

Ser Arg Trp Val Gln Arg Thr Lys Ala Arg Leu Gly Leu Ser Asp His  
545 550 555 560

Leu Pro Thr Phe Leu Ala Gly Leu Ala Ser Cys Thr Cys Arg Pro Phe  
565 570 575

Leu Ser His Leu Ala Gln Gly Asn Glu Asp Cys Val Gly Ala Lys Gln  
580 585 590

Ala Ala Val Val Gln Val Leu Lys Lys Leu Ala Thr Arg Lys Leu Thr  
595 600 605

Gly Pro Lys Val Val Glu Leu Cys His Cys Val Asp Glu Thr Gln Glu  
610 615 620

Pro Glu Leu Ala Ser Leu Thr Ala Gln Ser Leu Pro Tyr Gln Leu Pro  
625 630 635 640

Phe His Asn Phe Pro Leu Thr Cys Thr Asp Leu Ala Thr Leu Thr Asn  
645 650 655

Ile Leu Glu His Arg Glu Ala Pro Ile His Leu Asp Phe Asp Gly Cys  
660 665 670

Pro Leu Glu Pro His Cys Pro Glu Ala Leu Val Gly Cys Gly Gln Ile

675

680

685

Glu Asn Leu Ser Phe Lys Ser Arg Lys Cys Gly Asp Ala Phe Ala Glu  
690 695 700

Ala Leu Ser Arg Ser Leu Pro Thr Met Gly Arg Leu Gln Met Leu Gly  
705 710 715 720

Leu Ala Gly Ser Lys Ile Thr Ala Arg Gly Ile Ser His Leu Val Lys  
725 730 735

Ala Leu Pro Leu Cys Pro Gln Leu Lys Glu Val Ser Phe Arg Asp Asn  
740 745 750

Gln Leu Ser Asp Gln Val Val Leu Asn Ile Val Glu Val Leu Pro His  
755 760 765

Leu Pro Arg Leu Arg Lys Leu Asp Leu Ser Ser Asn Ser Ile Cys Val  
770 775 780

Ser Thr Leu Leu Cys Leu Ala Arg Val Ala Val Thr Cys Pro Thr Val  
785 790 795 800

Arg Met Leu Gln Ala Arg Glu Arg Thr Ile Ile Phe Leu Leu Ser Pro  
805 810 815

Pro Thr Glu Thr Thr Ala Glu Leu Gln Arg Ala Pro Asp Leu Gln Glu  
820 825 830

Ser Asp Gly Gln Arg Lys Gly Ala Gln Ser Arg Ser Leu Thr Leu Arg  
835 840 845

Leu Gln Lys Cys Gln Leu Gln Val His Asp Ala Glu Ala Leu Ile Ala  
850 855 860

Leu Leu Gln Glu Gly Pro His Leu Glu Glu Val Asp Leu Ser Gly Asn  
865 870 875 880

Gln Leu Glu Asp Glu Gly Cys Arg Leu Met Ala Glu Ala Ala Ser Gln  
885 890 895

Leu His Ile Ala Arg Lys Leu Asp Leu Ser Asp Asn Gly Leu Ser Val  
900 905 910

Ala Gly Val His Cys Val Leu Arg Ala Val Ser Ala Cys Trp Thr Leu  
915 920 925

Ala Glu Leu His Ile Ser Leu Gln His Lys Thr Val Ile Phe Met Phe  
930 935 940

Ala Gln Glu Pro Glu Glu Gln Lys Gly Pro Gln Glu Arg Ala Ala Phe  
945 950 955 960

Leu Asp Ser Leu Met Leu Gln Met Pro Ser Glu Leu Pro Leu Ser Ser  
965 970 975

Arg Arg Met Arg Leu Thr His Cys Gly Leu Gln Glu Lys His Leu Glu  
980 985 990

Gln Leu Cys Lys Ala Leu Gly Gly Ser Cys His Leu Gly His Leu His  
995 1000 1005

Leu Asp Phe Ser Gly Asn Ala Leu Gly Asp Glu Gly Ala Ala Arg  
1010 1015 1020

Leu Ala Gln Leu Leu Pro Gly Leu Gly Ala Leu Gln Ser Leu Asn  
1025 1030 1035

Leu Ser Glu Asn Gly Leu Ser Leu Asp Ala Val Leu Gly Leu Val  
1040 1045 1050

Arg Cys Phe Ser Thr Leu Gln Trp Leu Phe Arg Leu Asp Ile Ser  
1055 1060 1065

Phe Glu Ser Gln His Ile Leu Leu Arg Gly Asp Lys Thr Ser Arg  
1070 1075 1080

Asp Met Trp Ala Thr Gly Ser Leu Pro Asp Phe Pro Ala Ala Ala  
1085 1090 1095

Lys Phe Leu Gly Phe Arg Gln Arg Cys Ile Pro Arg Ser Leu Cys  
1100 1105 1110

Leu Ser Glu Cys Pro Leu Glu Pro Pro Ser Leu Thr Arg Leu Cys  
1115 1120 1125

Ala Thr Leu Lys Asp Cys Pro Gly Pro Leu Glu Leu Gln Leu Ser  
1130 1135 1140

Cys Glu Phe Leu Ser Asp Gln Ser Leu Glu Thr Leu Leu Asp Cys  
1145 1150 1155

Leu Pro Gln Leu Pro Gln Leu Ser Leu Leu Gln Leu Ser Gln Thr  
1160 1165 1170

Gly Leu Ser Pro Lys Ser Pro Phe Leu Leu Ala Asn Thr Leu Ser  
1175 1180 1185

Leu Cys Pro Arg Val Lys Lys Val Asp Leu Arg Ser Leu His His  
1190 1195 1200

Ala Thr Leu His Phe Arg Ser Asn Glu Glu Glu Gly Val Cys  
1205 1210 1215

Cys Gly Arg Phe Thr Gly Cys Ser Leu Ser Gln Glu His Val Glu  
1220 1225 1230

Ser Leu Cys Trp Leu Leu Ser Lys Cys Lys Asp Leu Ser Gln Val  
1235 1240 1245

Asp Leu Ser Ala Asn Leu Leu Gly Asp Ser Gly Leu Arg Cys Leu  
1250 1255 1260

Leu Glu Cys Leu Pro Gln Val Pro Ile Ser Gly Leu Leu Asp Leu  
1265 1270 1275

Ser His Asn Ser Ile Ser Gln Glu Ser Ala Leu Tyr Leu Leu Glu  
1280 1285 1290

Thr Leu Pro Ser Cys Pro Arg Val Arg Glu Ala Ser Val Asn Leu  
1295 1300 1305

Gly Ser Glu Gln Ser Phe Arg Ile His Phe Ser Arg Glu Asp Gln  
1310 1315 1320

Ala Gly Lys Thr Leu Arg Leu Ser Glu Cys Ser Phe Arg Pro Glu  
1325 1330 1335

His Val Ser Arg Leu Ala Thr Gly Leu Ser Lys Ser Leu Gln Leu  
1340 1345 1350

Thr Glu Leu Thr Leu Thr Gln Cys Cys Leu Gly Gln Lys Gln Leu  
1355 1360 1365

Ala Ile Leu Leu Ser Leu Val Gly Arg Pro Ala Gly Leu Phe Ser  
1370 1375 1380

Leu Arg Val Gln Glu Pro Trp Ala Asp Arg Ala Arg Val Leu Ser  
1385 1390 1395

Leu Leu Glu Val Cys Ala Gln Ala Ser Gly Ser Val Thr Glu Ile  
1400 1405 1410

Ser Ile Ser Glu Thr Gln Gln Leu Cys Val Gln Leu Glu Phe  
1415 1420 1425

Pro Arg Gln Glu Glu Asn Pro Glu Ala Val Ala Leu Arg Leu Ala  
1430 1435 1440

His Cys Asp Leu Gly Ala His His Ser Leu Leu Val Gly Gln Leu  
1445 1450 1455

Met Glu Thr Cys Ala Arg Leu Gln Gln Leu Ser Leu Ser Gln Val  
1460 1465 1470

Asn Leu Cys Glu Asp Asp Asp Ala Ser Ser Leu Leu Leu Gln Ser  
1475 1480 1485

Leu Leu Leu Ser Leu Ser Glu Leu Lys Thr Phe Arg Leu Thr Ser  
1490 1495 1500

Ser Cys Val Ser Thr Glu Gly Leu Ala His Leu Ala Ser Gly Leu  
1505 1510 1515

Gly His Cys His His Leu Glu Glu Leu Asp Leu Ser Asn Asn Gln  
1520 1525 1530

Phe Asp Glu Glu Gly Thr Lys Ala Leu Met Arg Ala Leu Glu Gly  
1535 1540 1545

Lys Trp Met Leu Lys Arg Leu Asp Leu Ser His Leu Leu Leu Asn  
1550 1555 1560

Ser Ser Thr Leu Ala Leu Leu Thr His Arg Leu Ser Gln Met Thr  
1565 1570 1575

Cys Leu Gln Ser Leu Arg Leu Asn Arg Asn Ser Ile Gly Asp Val  
1580 1585 1590

Gly Cys Cys His Leu Ser Glu Ala Leu Arg Ala Ala Thr Ser Leu  
1595 1600 1605

Glu Glu Leu Asp Leu Ser His Asn Gln Ile Gly Asp Ala Gly Val

1610

1615

1620

Gln His Leu Ala Thr Ile Leu Pro Gly Leu Pro Glu Leu Arg Lys  
1625 1630 1635

Ile Asp Leu Ser Gly Asn Ser Ile Ser Ser Ala Gly Gly Val Gln  
1640 1645 1650

Leu Ala Glu Ser Leu Val Leu Cys Arg Arg Leu Glu Glu Leu Met  
1655 1660 1665

Leu Gly Cys Asn Ala Leu Gly Asp Pro Thr Ala Leu Gly Leu Ala  
1670 1675 1680

Gln Glu Leu Pro Gln His Leu Arg Val Leu His Leu Pro Phe Ser  
1685 1690 1695

His Leu Gly Pro Gly Gly Ala Leu Ser Leu Ala Gln Ala Leu Asp  
1700 1705 1710

Gly Ser Pro His Leu Glu Glu Ile Ser Leu Ala Glu Asn Asn Leu  
1715 1720 1725

Ala Gly Gly Val Leu Arg Phe Cys Met Glu Leu Pro Leu Leu Arg  
1730 1735 1740

Gln Ile Asp Leu Val Ser Cys Lys Ile Asp Asn Gln Thr Ala Lys  
1745 1750 1755

Leu Leu Thr Ser Ser Phe Thr Ser Cys Pro Ala Leu Glu Val Ile  
1760 1765 1770

Leu Leu Ser Trp Asn Leu Leu Gly Asp Glu Ala Ala Ala Glu Leu  
1775 1780 1785

Ala Gln Val Leu Pro Lys Met Gly Arg Leu Lys Arg Val Asp Leu  
1790 1795 1800

Glu Lys Asn Gln Ile Thr Ala Leu Gly Ala Trp Leu Leu Ala Glu  
1805 1810 1815

Gly Leu Ala Gln Gly Ser Ser Ile Gln Val Ile Arg Leu Trp Asn  
1820 1825 1830

Asn Pro Ile Pro Cys Asp Met Ala Gln His Leu Lys Ser Gln Glu  
1835 1840 1845

Pro Arg Leu Asp Phe Ala Phe Phe Asp Asn Gln Pro Gln Ala Pro  
1850 1855 1860

Trp Gly Thr  
1865

<210> 187  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic primer

<400> 187  
tctcagctt aagagcagg

19